

chromodomain-helic
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
BH-protocadherin P
tenascin precursor
hypothetical prote
HAL5 protein - Yea
modifier-3 protein
probable proline-r
DNA-binding protei
spindle assembly C
C2BA5_6 protein (C
protein C2BA5_6 [I
hypothetical prote
probable WD-40 rep
En/Spm-like transp
hypothetical prote
hypothetical prote
M-protein - Helico
finger protein zfp
conserved hypothet
KTA622 protein -
unknown protein, 9

15 111.5 5.7 1711 1 A47392
16 107.5 5.5 395 2 T19144
17 107 5.5 561 2 T14792
18 106 5.4 447 2 T20552
19 105.5 5.4 857 2 T03552
20 105.5 5.4 1634 2 T26517
21 105 5.4 1200 2 T0042
22 105 5.4 1746 1 S19694
23 104.5 5.3 770 2 H94463
24 104.5 5.3 855 2 S56948
25 104 5.3 519 2 S23796
26 103.5 5.3 891 2 G84693
27 103.5 5.3 1203 2 S26650
28 103.5 5.3 1216 2 T09224
29 102.5 5.2 706 2 S43581
30 102.5 5.2 1061 2 G88428
31 102 5.2 560 2 T29586
32 102 5.2 925 2 T16235
33 101.5 5.2 451 2 T16418
34 101.5 5.2 932 2 T45894
35 101.5 5.2 1016 2 T25433
36 101.5 5.2 1269 2 T00443
37 101.5 5.2 1389 2 H84914
38 101 5.1 454 2 E84524
39 101 5.1 1252 2 T0263
40 101 5.1 1791 2 T02345
41 100.5 5.1 362 2 B64527
42 100.5 5.1 553 2 S22954
43 100.5 5.1 887 2 T39492
44 100.5 5.1 1289 2 T00387
45 100.5 5.1 1307 2 G96711

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
DeIop 6.0 , DeIext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=IR_79 -QFMT=fastan -SUFFIX=xLP -MINMATCH=0.1 -LOOPEXT=0
-UNITS=Bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human0.cdi -LIST=45
-DOCBLR=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfo -NORM=ext -HEAPSIZE=500 -MINLEN=20000000000
-USRP=US10046935 @CCN 1_1_46 @runat_12102004_155226_15255 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN THREADS=1 -XGAPOP=1.0 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -IGAPOP=0.5 -DEIOP=6 -DEIEXT=7
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Database : PIR_79:*

- 1: Pir1:*
- 2: Pir2:*
- 3: Pir3:*
- 4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	%
1	602.5	30.7	202	T50635	hypothetical prote	
2	289.5	14.8	462	D85438	hypothetical prote	
3	250.5	12.8	515	F56700	protein F12A21.9 [
4	170	8.7	555	T01142	hypothetical prote	
5	146	7.4	851	D66254	hypothetical prote	
6	142	7.2	950	F66222	hypothetical prote	
7	132.5	6.8	570	T49181	cyclophylin-like p	
8	131.5	6.7	906	T01440	hypothetical prote	
9	9	6.6	754	J05314	CDC28/cdc2-like ki	
10	117.5	6.0	595	T51747	RNA helicase RH26	
11	115.5	5.9	1701	T43213	ENBP1 protein - ba	
12	115	5.9	1051	G59436	KIAA1304 protein [
13	114	5.8	691	T48506	hypothetical Prote	
14	113	5.8	1641	T10955	early nodulin bind	

ALIGNMENTS

Result 1	DB:	Query Match:	Alignment Scores:
T50635			
hypothetical protein DKFZp762L0311.1 - human (fragment)			
Sp: Homo sapiens (man)			
Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004			
Accession: T50635			
Author: Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.			
Submitted to the Protein Sequence Database, June 2000			
Author: Reference number: Z25145			
Accession: T50635			
Author: Status: preliminary			
Molecule type: mRNA			
Residues: 1-202 <AA>			
Cross-references: UNIPROT:Q9NPV2; EMBL:AL359619			
Experimental source: adult melanoma (MeWo cell line); clone DKFZp762L0311			
Genetics:			
Author: Note: DKFZp762L0311.1			
Accession: T50635			
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Author: Note: DKFZp762L0311.1			
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Qy	223	AGTTTCCAGGCCGACTACCGGGSCAACACAAAGCAGTCGGCAAGGCC 282	A;Accession: T49181 B;Status: Preliminary A;Molecule type: DNA B;Residues 1-570 <RIB>
Db	18	AsnGluInThrArgSerAlaAsnGlyIleGlyAsnGlyIleSerIleProGly 37	A;Cross-references: UNIPROT:O9LY75; EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.30 A;Experimental source: cultivar Columbia, BAC clone MAA21 C;Genetics
Qy	283	TGAGAAATTGTGACTGATCTCAAATCGGTTCAAGAGT----- 324	A;Gene: ATSP:MAA21.30 A;Map Position: 3 A;Introns: 26/3; 45/1; 74/3; 83/1; 96/1; 135/2; 189/1; 341/2; 455/2; 482/2 F;6-175/Domain: cyclophilin homology <cyp>
Qy	325	-----GAAGTGAATGTTGGAGAAAGGGCTTTA 360	
Db	58	SerMetAlaAspLysThrValIcySgluLysHistYrlleGlnAlaIysLysargAlaIala 77	Alignment Scores: Preq. No.: 0.00363 Length: 570 Score: 132.50 Matches: 79 Percent Similarity: 39.09% Conservative: 41 Best Local Similarity: 25.73% Mismatches: 108 Query Match: 6.75% Indels: 80 DB: 2 Gaps: 15
Qy	361	AT-----ATAAAGAAAAAACGAAATGCTGGAAACTCATGCTGATTAA 408	US-10-046-935-2234 (1-1116) x T49181 (1-570)
Db	78	AsnSerAlaAsnGlyLysLysAlaLysAlaLysArgArgSerSerIleGlyIleThr 97	
Qy	409	GAAAGCTTCCCTGGCTCGTICGGAGAACATCCCTCCA----- 450	
Db	98	AspThr-TyrSerGluGlyLysMetAspAspPheGluLeuProValThrSerIleAspHis 117	
Qy	451	-----GGCTCCGACTACAATCAAGAGACCGGAAAGCTACA 489	Qy 4 GAGCTGCCTGGCTGGAGAAGATCTCAGAGTAAGAAACTTCAGATAAGAAATTCTAGA 63
Db	118	TyrAsnAsnGlyLeuAlaSerAlaSerIleAspSerIleAsp 137	Db 207 GluAlaIysGluThrArgLysIysGluSerIleAsnGlyIleSargLysArg 226
Qy	490	TTCCCCTGGCTGCTCCAGGAGAACCTGAAACGGAGGCTGCTCACCGCTCA 549	Qy 64 TAGTGAGATGATTCATGGAAAACCTCGNATCATCTCTGTGACAGTTGTGACAGC----- 120
Db	138	-----LyserSerLeuMetArgTyrSerProGlu-----ThrProMetMetArgSer 152	Db 227 TyrSerSerSerAspSerSerSerAspSerAspSerAspSerAspSerAspSerAsp 246
Qy	550	AGGTCC---CGATCTCTGGTCCCTT---GAGCTCTACCCATGRRGAGGCCAGTTK 603	Qy 121 ---TTTCCTCTGTATAATTGCAAACQAGGGCTGCACTTAGTGGAGGGCTCTAG 177
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Qy	604	GARKMTNWGIACATGTGGTGAGAAAGACCGTGGATCATGAATGAGAGT 663	Qy 178 ACCGCAAGCCAGTGCKAGACTCTGCAACCTCTCAGGGTGGCATGAGAATTCAGCCGG 237
Db	173	GluGluGlyTyrArgSerTyrArgThrProProSerVal---AlaValMetAsp----- 189	Db 267 ---LysSerThrThrGlyIleSlysGly-----ArgArgGlyIleArg 279
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Db	202	MetGlu-----TyrSerAlaAlaSerThrAspVal 211	Db 300 SerSerSerAspThrGluUserSerSerSerAspAspGluLys-----Val 315
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Db	232	IleSerIleLysCysSash-----GinargAlaPheYshiasnCysSleu 247	Db 342 SerArgSerProIlePheIg-----ArgArgAsnGlnAsnSer 353
Qy	904	CGAAAACCGTTATGCTGGATGCTCTGCTGGTGGATCGAAC 951	Db 348 -----SerValIysSerIleGluGluIvaIgluLysVal-----SerArgSerProValArg 379
Db	248	SerAlaArgTyrSerGiuIleSerIleGluGluIvaIgluLysVal----- 262	Qy 526 AGAGCTGCTCTCTACAGTCAGGCTCCGGATCTCGGGCTCTTGAGCTCTAACCC 585
Qy	952	TGGCATGGCCGCCCTGAGGAACTGCAACTGAGTTCTGGCTGGCAACGGAGT 1008	Db 354 ArgSerIysSerProSerArgSerProArgSerProArgSerPro 373
Db	263	-----CysProAlaCysArgGlyIleLeuCysAspCysLysSerCysLeuArgSerAsp 279	Qy 586 ATGGRGAGCCAGCTGKTMWGTACATGTTGAGAACGAGGAGACCGTGGAT 645
RESULT 7			Db 374 -----SerArgSerProValArg 379
T49181		cyclophillin-like protein - Arabidopsis thaliana	
N;Alternate names: Protein MAA21.30		C;Species: Arabidopsis thaliana (mouse-ear cress)	Qy 646 GGCTACATGAATGA----AGAGTACCTGCCAGAACGCGTGCCTCGCATCGTGC 701
C;Date: 02-Jun-2000 #Sequence_revision 02-Jun-2000 #text_change 09-Jul-2004		Db 380 AspLeuIysArgLysSerProArgSerProArgSerProArgSerPro 399	
C;Accession: T49181		Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, R.	702 CCTTCCGCATAATACTGCCAGTGG-----AGAAATTACAGGGAGGAGTGGAA 755
submitted to the Protein Sequence Database, April 2000		A;Reference number: 225018	Db 400 SerPheArgSerProSerProSerGlyValProlysArgleArglysIysArgGly----- 418

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b	457 LysSerLysSerArgSerLysSerLysGluLysSerLysGluArgAspSerLys 476	
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b	477 HisSerArgAsn----- 506	-GluGluLysArgMetArg 486
Y	184 AGCCGCTGCGGGCATCTGACCTCTCAGGGGGATGAAGTTCAACGGGAGTACC 243	: :
b	487 SerArgSerLysGluArgSerLysSerLysGluLysSerLysGluAspSer 506	: :
Y	244 AGGGAGCAACCAACAAAAAGCAGACTCCGCCAGCCCCCTCAGAAATTCTGTGACTGAT 303	: :
b	507 LysGluLysAspGluLysSerLysGluLysSerLysGlu-----LeuGlu 524	: :
Y	304 TCCACTCTGGATTGCAAGATGAAAGTGGATGAACTTGGAAQARANGGCTTAAAT 363	: :
b	525 SerLysSerAsnGluHisAspHisSerLysSerLysGluLysAspArgArgAla----- 542	: :
Y	364 ATAAGCAAAACAAAGCAATGCTGCAAAACTATGTCGAATTAAGAAAGCTTCTGGC 423	: :
b	543 ----GlnSerArgSerArgGluLysAspThrLysSerLysSerAsnSer 560	: :
Y	424 TCGTCTGGTGAAGACATCCCTCCAGGGCTCGACTCACAACTAGGAGACCCGAAAGC 483	: :
b	561 ArgThrArgLysArg-----SerArgSerArgAspArgSerLysArgValArgSer 577	: :
Y	484 CGTAACTTCCCGGGCTTCTCCGG-----AGAAACCTGAA 522	: :
b	578 ArgThrHisAspArgAspArgSerArgSerLysGluTyroSleutYrhIsArgTyraGluGlnGlu 597	: :
Y	523 CGGAGAGCTCTCCCTTACAGGTCAAAGTCCCGATCTCGGCTCCCTTGACGCTCTA 582	: :
b	598 TyrArgArgGlyLysArgSerArgSerArgGluArg-----ArgThr 611	: :
Y	583 CCCATGGRGAGGCCAGTTKGARNMTMNGTACATGTTGAGAAAGGAAAGACCGCTG 642	: :
b	612 ProProlglySerArgSerLysAsp-----ArgGargArgArgArg 626	: :
Y	643 GATGGCTACATGAGTGAAGATGACTGCCAGAACCGTGCTCAGATCTCGTGAC 702	: :
b	627 AspSerArgSerSerGluArgGluLysSerGlnSerArgAsnLysAspLys----- 643	: :
Y	703 CTTCCGCATAATAUTGCCCAAGTGGAGAAATTAGAGGAGGAGATTGAGAAACCTCTGC 762	: :
b	644 -----TyrArgArgGlnGluLysSerLysSerLysSerLysGluAsn----- 657	: :
Y	763 AGCAATTCTCGAGAGAAAGATAAACCGTTCACTGGGC-----TCTACTCTGTCATGATGC 819	: :
b	658 SerGluUserGluLysArgMetArgSerLysSerArgAspHisSerAsnSer 677	: :
Y	820 CGTCAGAAGCTATGATGAT-----ACCAAAACAAACTCCGAAACCA 861	: :
b	678 ArgGluLysAlaAspArgAspGlnSerProHeSerSerLysGlnSerGln 697	: :
Y	862 GACTGCTGGGGCTGAGGCACTCTGTCGATCGATCGATCGAAC 921	: :
b	698 Asp-----AspGluLysSerSerMetLeuLysAsnLysGluAspGlu 712	: :
Y	922 GAGGTCAGGGATGCTCTGCTGATCGAAC 951	: :
b	713 LysLysArgSerSerValGluLysGluAsn 722	: :

A;Title: The DEAD box RNA helicase family in <i>Arabidopsis thaliana</i> .	
A;Reference: Z22965 ; MTID:9822990 ; PMID:9862990	
A;Accession: T51747	
A;Status: preliminary; translated from GB/EMBL/DDJB	
A;Molecule type: mRNA	
A;Residues: 1-955 <A>	
A;Cross-references: UNIPROT:Q9ZRZ9 ; EMBL:AJ010474 ; PIDN:CAA09213.1	
A;Experimental source: cultivar Columbia	
C;Genetics:	
A;Gene: RH26	
A;Map position: 5	
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Alignment Scores:	
Pred. No.:	Length: 595
Score:	Matches: 73
Percent Similarity:	Conservative: 37
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Query Match:	Indels: 96
DB:	Gaps: 15
US-10-046-935-2234 (1-1116) x T51747 (1-595)	
Qy	6 CGCTCGCGCTGCCAGAAAGATCTAGAGTAAAGAGACTTAAAGAAA
Db	41 Arg Gly Pro Arg Garg Gly Arg Glu Gly Gln Ser Asp Arg -
Qy	66 TGTGAAGTTGATTCCATGGAAACCTGTCACTCTGTATGAAGTTGTGAC
Db	54 --- Phe Gly Gly Ala Lys Arg Gly Lys Glu Gly Lys Glu Met Asp
Qy	126 TTCT-----GATAATTTGCAAAAC
Db	69 ySer Pro Asn Arg Arg Arg Gly Glu Pro Ala Asp Ser Gly Lys Asn Ile
Qy	153 GCAGTCAGTTGCCGAGGCTTGAGCCCCAACCGTAGCGGCACACTGAGA
Db	89 ugly Asp -- Arg Glu Gly Ser Arg Asn Gly -
Qy	213 GETGGCGATGAGTTCCAGGGGAGTACCAAGGGAAACCACCAAAAAAA
Db	99 gVal Glu Gly ySer Ser Gly Ser Ser Phe Arg Gly Arg Ser Asp Arg Asn
Qy	273 C-----CGCACGCCCTCAGAGAACATTCGTGACTGATCCAACTCC
Db	119 rGly Ser Ser Phe Arg Gly Arg Ser Gly Ser Gly Ser Ser Ile
Qy	313 -----GATTGAGAATGAGCTGAAATGATTTTTGAGAAGGGCTT
Db	139 Y Arg Asn Asp Arg Asn Val Asp Ser Gly Ser Ser Phe Arg Gly Arg Ser Asp
Qy	366 AAAAGCAAAACAAGCAATGCTGCAAAACTCATGCTGAATTTGAAAGTTC
Db	159 IAsp Ser Gly Ser Ser Phe Arg Gly ySer Ser Arg Ser Val Asp Ser --
Qy	426 GTTCGGTGGAAAGAACATCCCTC-----CCAGGGCTCGACTCACATCA
Db	178 rPhe Arg Gly Arg Asn Asp Arg Asn Val Asp Ser Gly Ser Ser Phe Arg Gly
Qy	477 GCGAAG-----GCTACATTCCCGGGTTGCTCCAGAGAA
Db	198 pArg Asn Val Glu Ser Gly Phe Arg Arg Glu Pro Gly Ser Gly Asn Arg Ser Asp
Qy	522 ACGGAGGCTCTCTCTTAC-----AGGTCA
Db	218 yLys Glu Ser Gly Leu Ser Ieu Glu Glu Glu Asp Ser Ser Asp Asp
Qy	558 GATC--CTCGGGTCCCTTGACCTCTAACCCATGGAGAGCCAGT-----
Db	238 gVal Gly Leu Gly Asn Ile Asp Asp Leu Pro Ser Glu Asp Ser Ser Asp Glu
Qy	606 RKRMTNGTACATGTTGGTGAAGAAAGG-----

Db	258 uAsnAspGluProLeuIleLysLysAlaAlaLysSerAlaLysAlaValGlnThrAspLySPr	278	Qy	559 ATCCCTCGGGTCCCTTGACGCTCA-	582
Qy	634 -----AAGACCCGTGGCTACATGATGAA-----GATGACT	668	Db	753 ValAspGluAlaIeuSerThrIleIvalProHisLysIleGluSerIleSer 772	
Db	278 oHrglyGluHisvallysthserserAspserTyLeuserIysThrArgPheAspGlnPh	298	Qy	583 -----CCATGGRGAGGCCAGTTGKARMTMGTACATGTTGGTGGAGAG 630	
Qy	669 GCCCAGAGGCCGCGTCAGATCATCCGT-----	699	Db	773 ProLeuLysAspProValAsnLysGluLysSerIysSerPhenValLeuGlucySerLys 792	
Db	298 eProLeuSerProLeuSerLeuLysAlaLysAspAlaGlyPheGluThrMetThrva	318	Qy	631 -----AGAAAGACCCGTGGCTACATGATGAAAGATGACCTGCCAGAGC 678	
Qy	700 -----ACCCCTCCGATATAATTTCGC	720	Db	793 AspSerGlyIleGluLysIleThrLysLeuMetSerLysSerGlyAspValHisLys 812	
Db	318 IValGlnGluAlaThrLeuProIleLeuGin	329	Qy	679 CGTGCCTCCAGATCATCGTGAACCTTCGGCATATAATTGCCAGTGGAAAGATA 738	
RESULT 11					
T43213	ENBP1 protein - barrel medic		Db	813 ArgCysSerGluArgLeuArgIleLeuThrAspHisLysSerGlnAspValGlu	832
N	Alternative names: chloroplast-localised DNA-binding protein PD3 homolog		Qy	739 GAGGAGGAGTTGGAAAGCTCTGAGAGAAATATAACCGTTCAGTCAG 798	
C	Species: Medicago truncatula (barrel medic)		Db	833 ValGlu-----GluThrPheCysGluAsnGluValGluIuaAlaIleAspHisGluLeu	850
C	Date: 11-Jan-2000 #Sequence_revision 11-Jan-2000 #text_change 09-Jul-2004		Qy	799 GGCTCTACT-----TGT 810	
R	Christianen, H.; Barker, D.G.		Db	851 GluSerSerAspLeuMetGlyGluProGluThrLysGluProArgAsnLeuArgCys	870
A	Submitted to the EMBL Data Library, October 1997		Qy	811 CATCAAATGCCGTCAGAAGACT-----ARTGATACCAAAACAAACTGCGAGAACCA 861	
A	Accession: T43213		Db	871 HisGlnCysTrpLysSlySerArgThrGlyIleValValValYstHylCysLys----- 888	
A	Status: preliminary; translated from GB/EMBL/DBJ		Qy	862 GACTGCTGGGGCTCTCAGGCCAGTGTGCCCCCAGCTTGAAACCGTATGGTCAA 921	
A	Molecule type: DNA		Db	889 -----ArgLysIstSlyCysTrpGlycylsleAlaLysIstTrpTrpGlnAsp 903	
A	Residues: 1-1701 <C-TR>		Qy	922 GAGTCAGGGATGCTCGCTGATGCCAACTGCGCATGCCGCTTGCGAGAATCTG 981	
A	Cross-references: UNIPROT:082022; EMBL:AU002479; NID:e1317985; PID:e1317986; PIDN:CRAC0		Db	904 LysThrArgGluGluIle-----GluThrAlaCysProPheCysLeuAspTrpCys	920
A	Experimental source: cultivar Jemalong		Qy	982 AACTGCAGCTTCTGCCCCCAGGAGATGGACGGTGTGCGACTGGGTCTTGTTTA 1041	
C	Genetics:		Db	921 AsnCysArgLeuIysIstLeuIysIstThr-----Ile 930	
A	Gene: ENBP1		Qy	1042 GCCAAATATCATGGCTTGGGAATGTGCTACTTGAAAGCTGAAA 1092	
A	Introns: 856/3; 900/2; 933/3; 978/1; 1000/2; 1220/3; 1329/3; 1565/3; 1610/1; 1638/3; 1		Db	931 SerThrMetAsnCysAsnGlyGluIuaAspAlaAspValIysLeuGinLys 947	
RESULT 12					
Alignment Scores:					
Pred. No.:	0.122	Length:	1701		
Score:	115.50	Matches:	70		
Percent Similarity:	32.77%	Conservative:	47		
Best Local Similarity:	19.61%	Mismatches:	129		
Query Match:	5.89%	Indels:	111		
DB:	2	Gaps:	13		
US-10-046-935-2234 (1-1116) × T43213 (1-1701)					
Qy	244 AGGGAGGACCACAAAGAGTAGTCGCCAGCCTAGAGAATCTGACTGAT	303	Qy	59436 KIAA1304 protein [Imported] - human	
Db	628 LysGlySerLysIasnLysLys-----	634	C	Species: Homo sapiens (man)	
Qy	304 TCCAACTCGATTCAAGATGAAAGTGAATGAAATTGAGAAAAGG-----	354	C	Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004	
Db	635 LysAsnIleAlaGlyGluAspGlyAsnIleSluHisIysGluLysSlySargArgGlyIrp	654	C	Accession: H59436	
Qy	355 -----GCTTAAATAATAAAACAAACAAACTGCTGAAACTCATGCT	402	R	Nagase, T.; Kikuno, R.; Ishikawa, K.I.; Hirose, M.; Ohara, O.	
Db	655 ProLySgIyPheCysLeuLysProLysProLysLeuAlaIleAlaArgLeuAspGluLysIleGlu	674	DNA Res.	7, 65-73, 2000	
Qy	403 GATTAGAAGCTCCGGCTACATCCGGGTGTGGTGAAGATCCGGCTCGACTCA	462	A	Title: Prediction of the coding sequences of unidentified human genes . XVI . The complete genome sequence of human chromosome 22.	
Db	675 ArgArgGlyArgProLySgIySer-----GlyMetLysProLySgIuThrAlaValGln	692	A	Reference number: G59436	
Qy	463 CAACTAAAGGAGCCGGCTACATCCGGGTGTGGTCCAGGAGA-----	513	A	Accession: H59436	
Db	693 LeuAspAlaLysIleGluArgGlyIlysLysProLySgIyLys 712		A	Molecule type: mRNA	
Qy	514 -----AACCCCTAACGGAGGCTCGTCCTCT-----	540	A	Residues: 1-1051 <OHA>	
Db	713 IleValValArgLeuAspThrLysIleGluArgGlyIysProLySgIyLys 732		A	Cross-references: GB:BAA92542; PID:97242963; PIDN:BA92542.1	
Qy	541 -----ACCAGTCAGGTCCCG 558		Alignment Scores:		
Db	733 LysGlnLysGluValAlaSerGinLeuAlaLeuGlnIleGluSerGinLysserThrArg	752	Pred. No.:	0.127	
			Score:	115.00	Length:
			Percent Similarity:	31.70%	Matches:
			Best Local Similarity:	19.85%	Conservative:
			Mismatches:	129	

		Best Local Similarity:	20.28%	Mismatches:	125
		Query Match:	5.76%	Indels:	118
		DB:	2	DB:	17
		US-10-046-935-2234 (1-111) × T10955 (1-1641)			
Db	318 LysLysBAlaGlnGluAsnAspValLeuLysGlnLeuThrLysGlnLysSerMetProAla 337				
Qy	565 GGG-----TCCCCITGACGCCCTACCCATGGRGAAGGCCAGT 600				
Db	338 GlyGluArgTy-SerGlnGluUserSerSerDlyLeuAspaspArgProLeuLysSrglInLys 357				
Qy	601 TTKGARKMTMMGTACATGGT-----GTGACAAGAAGGGAAACC 639				
Db	358 LeuAspGlySerValThrValArgAspClyTrpAspThrThrIleLeuAsnIleThr 377				
Qy	640 GTGGATGCGCTACATGAAATGAAATGACCTGACCGTCAGATCATCGTG 699				
Db	378 SerAspGly-----LysLysAspThrGlySerPheLeuArgProArgAspLysVal 394				
Qy	700 ACCCTTCGGCATATAATTGCCCAAGTGAAAGAAATTACAGAGGAGGTGGAAACGTC 759				
Db	395 Thr-----IleGluGluValProProGluTy-BArgSerPheVal 407				
Qy	760 TGCAGCAAATTCTCGAGAGAGATATAAACCGTTCACTGGCTCTACTGTGTCATCATGC 819				
Db	408 -----LysAsnArgAspLeuValValSerValSerGlyLysThrLysThrVal 425				
Qy	820 CGTCAGAAGACTATTGATCACAAACAAAC-----849				
Db	426 ThrGluLysGlyLeuSerLysSrglProSerPheGlyArgAlaGluAspLysMetSerAla 445				
Qy	850 -----TGAGAAACCCAGACTGCTGGGC 873				
Db	446 AspAspAsnGluArgAsnTyRglnValThrGluValCysArgAtpGtPAspAlaArgVal 465				
Qy	874 GFT-----CGAGCCCAAGTCCTGGCCCTCTGCGCTTCGAACCGTTATGGT 918				
Db	466 ValLyserSerLeuAspAlaArgMetTrpPhePheSrglAsnThrIle-----480				
Qy	919 GAAGAGGTCAGGGATGCTCTGCTG-----GATCCGAACACTGGCTACATGCCGCCCTTGTCA 972				
Db	481 -----LeuLysGlyAlaValleuPheTySerProSer---HisCysMet-----494				
Qy	973 GGAATCTGCAAATGCAACTTCTGCGCAGAGATGACGTGGACTGGGTCTT 1032				
Db	495 ---LeuTySerSerCysSer-----AspValLeu 502				
Qy	1033 GTCATTTAGCCAAATATCAT-----GCTTTCGGAAATGTCATGCCCTACTTGAA 1083				
Db	503 SerPhePheSerSerTyTyValThrThrMetLeuGlyAspIleGluProTrpGlu 522				
Qy	1084 AGCCTGAAACAG 1095				
Db	523 SerMetArgGlu 526				
RESULT 14					
T10955	early nodulin binding protein 1 - spring vetch C;Species: Vicia sativa (spring vetch, bare) C;Accession: 16-Jul-1999 #sequence_change 09-Jul-2004				
Db	Submitted to the EMBL Data Library, December 1995 A;Description: A novel type of DNA binding protein interacts with a conserved sequence i A;Accession number: Z17228 A;Status: preliminary; A;Molecule type: mRNA A;Residues: 1-1641 <CHR> A;Cross-references: UNIPROT:Q41700; EMBL:X95995; NID:gi1360633; PID:e225826				
Qy	R;Christiansen, A.; Hansen, A.C.; Vijn, I.; Pallisgaard, N.; Larsen, K.; Yang, W.C.; Biess A;Accession: T10955 A;Accession number: Z17228 A;Status: preliminary; A;Molecule type: mRNA A;Residues: 1-1641 <CHR> C;Genetics: A;Note: ENBP1 C;Keywords: DNA binding				
Db	Alignment Scores: Pred. No.: 0.199 Score: 113.00 Percent Similarity: 32.50%				
Qy	Length: 1641 Matches: 73 Conservative: 44				
Db	886 TTCTGTCGCCCTGCCCCTGCAAACCGTTATGGAAAGGGATGCTGCTGCTGAT 945 837 TyrCysTyrGluCysValAlaLysTrpTyrlnAspLysThrArgGluLile-----854				
Db	832 -----ATTGATACCAAACAAACTGCAAGAACCCAGACTCTGGGGCTGTCAGGCCAG 885 824 ThrGlyIleValValCysSerLysCysLys-----LysLysLys 836				

Qy	946 CGAACTGGATTGCCGCTTGCGGAAATCAGCACTGAGTTCTGCCGGAGCGA	1005	Qy	463 CAATCAGGAGACCCGA---AGGGTACATTCCGGTTGCCTTCAGGAAACCC	519
Db	855 --GluthrAlaCysProPheCysLeuAspTyrcAsnCysArgMetCysLeuLysLys	873	Db	164 GluSerGluGluGluArgAspLysSerCysAspGlyThrGluSerAspTyrgluPro	183
RESULT 15			Db	164 GluSerGluGluGluArgAspLysSerCysAspGlyThrGluSerAspTyrgluPro	183
A47392	chromodomain-helicase-DNA-binding protein, CHD-1 - mouse		Qy	520 GAACGGAGAGCTCT---CCTCTTACAGGTCAAGGTCC-	558
N;Alternate names: KYBP protein	Species: Mus musculus (house mouse)		Db	184 LysAsnLysValArgSerArgLysProGlnAsnArgSerLysSerLysAsnGlyLysLys	203
C;Accession: A47392 ; S21568	Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Dec-2002		Qy	559 ATCCCTGGTCCCTGACGTCTACCATGAGCCAGTTKGARANTMMGTACATG	618
R;Delmas, V.; Stokes, D.G.; Perry, R.P.			Db	204 IleLeuGly-----	206
Proc. Natl. Acad. Sci. U.S.A. 90, 2414-2418, 1993			Qy	619 TTGGTAGAAAGGAGAACGGTGGTACATGAAAGATGACCTG-----	669
A;Reference number: A47392 ; PMID:9311972; PMID:8460153			Db	207 -----GlnLysLysArgGlnIleLeuAspSerGluAspLysAspGluAspTyraasp	224
A;Accession: A47392			Qy	670 -----CCCAGAACGGCGTCCGATCAGATCATCCGTGACCCCTCCGCATAATAATTGCCCA	723
A;Species: prelimary			Db	225 AsnAspLysArgSerSerArgGlnIleLeuAspGluAspGlu	244
A;Molecule type: mRNA			Qy	724 GTGGAGAAATTACAGGGAGGTGGGAAACGCTGCGAACATTCTCGAGAGAGATA	783
A;Residues: 1-1711 			Db	245 GluMetLysThrAspSerAspPheLeuGluValCysGlyGluAspValProGlnPro	264
A;Experimental source: S194 plasmacytoma cell line			Qy	784 TATAACGGTCACTGGCTACTGTCAATGCCGTAGAAACTATTGATAACAAA	843
A;Note: sequence inconsistent with the nucleotide translation			Db	265 GluAspGluGluPhe-----	275
A;Note: sequence extracted from NCBI backbone (NCBIN:128272, NCBIPI:128273)			Qy	844 ACAAACTGCAGAACCCAGACTGCTGGGGCTCGAGGCCAGTCTGTGCCCTGCCTT	903
R;Delmas, V.; Perry, R.P.			Db	276 MetAspCysArg-----	289
A;Cross-references: EMBL:X66028			Qy	904 CGAAACCCTPATGGTAAGGGTCGGATCGGATCTGGCATGGC 963	
C;Submitted to the EMBL Datab Library, May 1992			Db	290 ThrThrLysThrAlaValGluAlaAspGly-----	
A;Description: KYBP, a mammalian protein that contains the SNF2/SWI2 helicase domain also			Qy	964 CCTTGTGAGGAATCTGCAACTGCAGTTCTGGCGAGGATGGACGTTGTGGACT	1023
A;Accession: S21568			Db	302 -----AsnAlaGlyPheGluArgAsnLysGlu-----	311
A;Molecule type: mRNA			Qy	1024 GGGTCCCTGGTATTAGCCAATATCATGGCTTGGGATGTGGCT	1074
A;Residues: 777-1711 <DE2>			Db	312 GlyAspGlnTrpLysLysIleLeuAspGly-----	
A;Cross-references: EMBL:X66028			Qy	1075 TACTGAAAGCCTGAAACCGAA	1098
C;Keywords: chromodomain helicase CHD1; chromobox homology			Db	332 ThrGluGluThrLeuLysGinGin 339	
F;293-336/Domain: chromobox homology <CB1>					
F;387-427/Domain: chromobox homology <CB2>					
Alignment Scores:					
Score: 0.27	Length: 1711				
Percent Similarity: 11.50	Matches: 82				
Best Local Similarity: 38.04%	Conservative: 58				
Query Match: 5.68%	Mismatches: 133				
DB: 1	Indels: 95				
	Gaps: 1.8				
US-10-046-935-2234 (1-1116) x A47392 (1-1711)					
Qy	79 TCCATGGAAACCTCGTATCCTCTGTGACGTTGACAGCTTGATATAATT	138	Qy	1075 TACTGAAAGCCTGAAACCGAA	1098
Db	39 SerAspGlySerSerGlnSerGlySerSerGlnSerGlySerSerAsp-----	55	Db	332 ThrGluGluThrLeuLysGinGin 339	
Qy	139 GCAAAACAGGAACTCGAGTCACTTCCGGAAAGCTGTAGGACCCGCCACTGCAAGCAC	198			
Db	56 SerAspSerGlySerGlnSerGlySerSerGlnSerGlySerSerAspThrSerArgLysValGln	75			
Qy	199 TCTGGACCTCTCAGGCTG---GCGTAGAACGTTCCAGCGGCCAGT	240			
Db	76 AlanLysoProLysAlaLeuGluPheTriPheSerProSerIleLeuAla	95			
Qy	241 ---ACCAAGGGCAACCAAAMA-----GAGAGTCGGCAGGCC	282			
Db	96 ValGlnArgSerAlaLeuArgLysGlnProGlnGlnAlaGlnGlnGlnGlnArgProAla	115			
Qy	283 TCAGAGATTCTGTGACTGTTCCAATCCGATTCAAGAGTAACACTGGAAATGAAATT	342			
Db	116 SerSerLysSerGlySerGluGluAspSerSerSerGluAspSer-----	131			
Qy	343 TTGGAGAAAGGGCTTAATAAACAAACAAAGCAATCTGCAAACACTCATGTC	402			
Db	132 ---AspAspSerSerGlyAlaLysLys-----His 143				
Qy	403 GAATTAAGGATTCCCTGGCTTCGAGAGACATCCCTCCAGGCTCCGACTCA	462			
Db	144 AsnAspGluAspTrpGlnMetSerGlySerGlySerProSerGlnLeuGlySerAspSer	163			

Search completed: October 12, 2004, 15:19:50
Job time : 43 secs

Blank

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6
OM nucleic - protein search, using frame_plus_n2p model	
Run on:	October 12, 2004, 15:05:41 ; Search time 171.5 Seconds (without alignments)
Title:	US-10-046-935-2234
Perfect score:	1962
Sequence:	1 atggacgctcgccgtgcc.....aaatttggaaatgcggcaagctaaa 1116
Scoring table:	BLOSUM62
Ygapop 10.0 , Xgapext 0.5	Ygapop 10.0 , Ygapext 0.5
Egapop 6.0 , Egapext 7.0	Egapop 6.0 , Egapext 7.0
Delop 6.0 , Delect 7.0	
Searched:	1825181 seqs, 575371646 residues
Total number of hits satisfying chosen parameters:	3650362
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	

Command line parameters:

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-O=/sgn2.1/USP0_spool_p/IS10046935/runat_12102004_155225_15243/15243.ipb_query.fasta_1.1287
-DB=DiniProt_02 -QFMT=fastian -SUFFIX=rup -MINATCH=0..1 -LOOPENXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-DOCLIGN=200 -THR SCORE=ECT -THR MAX=100 THR MIN=0 -ALIGN=15 -NODE=LOCAL
-OUTFMT=pfo -NORM=ext -HEAPSIZ=500 -MINLEN=2000000000
-USERUS10046935@CGN 1..183 @runat_12102004_155225_15243 -NCPU=6 -TCPU=3
-NO_NMAP -LARGEQUERY -NEG_SOURCES=0 -WAIT_DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : UniProt_02:
 1: uniprot_sprot;
 2: uniprot_trembl;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1929	98.3	Q9bwt1	Q9bwt1 homo sapien
2	1879.5	95.8	Q56SP5	Q56SP5 homo sapien
3	1612.5	82.2	Q9DM2	Q9DM2 m mus musculus
4	1609.5	82.0	Q9NZES	Q9NZES mus musculus
5	1609.5	82.0	AHH66169	AHH66169 mus musculus
6	1607.5	81.9	Q8CIAO	Q8CIAO mus musculus
7	1155	58.9	Q96BV8	Q96BV8 homo sapien
8	786	40.1	Q9NBV9	Q9NBV9 homo sapien
9	752	38.3	Q96C70	Q96C70 homo sapien
10	752	38.3	Q86YTO	Q86YTO homo sapien
11	752	38.3	AHH25242	AHH25242 homo sapien
12	752	38.3	Q96GN5	Q96GN5 homo sapien
13	743	37.9	Q6P14	Q6P14 homo sapien
14	743	37.9	AH32576	AH32576 homo sapien
15	736	37.5	Q922M5	Q922M5 mus musculus
16	602.5	2	Q9NPV2	Q9NPV2 homo sapien

ALIGNMENTS

ID	Q9bwt1	PRELIMINARY;	PRT;	371 AA.
AC	Q9bwt1;			
DT	01-JUN-2001 (TRIMBLrel. 17, Created)			
DT	01-JUN-2001 (TRIMBLrel. 17, Last sequence update)			
DT	01-OCT-2004 (TRIMBLrel. 28, Last annotation update)			
DE	C-Myc target JPO1 (cell division cycle associated protein 7, isoform 2) (Hypothetical protein FLJ14736).			
DE	Name=JPO1; Synonyms=CDCA7;			
GEN	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TAXID=9606;			
RN	[1] -	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21611205; PubMed=11598121;			
RA	Prescott J.E., Osthus R.C., Lee L.A., Lewis B.C., Shim H.-Y., Barrett J.F., Guo Q., Hawkins A.L., Griffin C.A., Dang C.V.; "A novel c-Myc-regulated gene, JPO1, participates in neoplastic transformation." J. Biol. Chem. 276:48276-48284 (2001).			
RL	[2]	SEQUENCE FROM N.A.		
RP	TISSUE=Pancreas; MEDLINE=2238825; PubMed=12477932;			
RX	Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shearer C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaeetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Hellton E., Kettman J., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko K.Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			

Rodríguez A.C.,	Grimwood J.J.,	Schmutz J.,	Myers R.M.,	Butterfield Y.S.,
Krzewinski M.I.,	Skalska U.,	Smallius D.E.,	Schnurch A.,	Schein J.E.,
Jones S.J.J.,	Marra M.A.,	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";		
Proc. Natl. Acad. Sci. U.S.A.	99:16899-16903 (2002).			
[3]	SEQUENCE FROM N.A.			
RP	RP	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.		
RN	RN			
SEQUENCE FROM N.A.				
PubMed=14702039;				
RX	RX			
RA	RA	Nishikawa T., Otsuki T., Sugiyama T., Irie R.,		
RA	RA	Ota T., Suzuki Y., Nishikawa T., Sato H., Nagai K., Kimura K., Makita H.,		
RA	RA	Wakamatsu A., Hayashi K., Nishi T., Shibahara T., Tanaka T., Ishii S.,		
RA	RA	Sekine M., Obayashi M., Nishi T., Shiratori A., Nagahara Y., Nagahara K.,		
RA	RA	Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,		
RA	RA	Murakami K., Iwayanagi T., Wagatsuma M., Shiratori A.,		
RA	RA	Sudo H., Hosoi T., Karu Y., Kodaira H., Kondo H., Sugawara M.,		
RA	RA	Takahashi M., Kanda K., Yokoi T., Furuya T., Omura Y.,		
RA	RA	Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,		
RA	RA	Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,		
RA	RA	Tanai H., Kimata M., Watanabe M., Hirada S., Chiba Y., Ishida S.,		
RA	RA	Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotta T., Kusano J.,		
RA	RA	Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,		
RA	RA	Togita S., Konai F., Hara R., Takeuchi K., Arita M., Imose N.,		
RA	RA	Masushino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,		
RA	RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,		
RA	RA	Moriya S., Moriyama H., Satoh N., Takami Y., Terashima Y., Suzuki O.,		
RA	RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakae H.,		
RA	RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,		
RA	RA	Yamamoto M., Watanabe K., Kumagai A., Fukuzumi Y.,		
RA	RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,		
RA	RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,		
RA	RA	Rakuda A., Hikiji T., Kobuchi H., Inagaki H., Ikeda Y., Okamoto S.,		
RA	RA	Okitani R., Kawakami T., Nozuchi S., Itoh T., Shigeoka K., Semba T.,		
RA	RA	Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,		
RA	RA	Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,		
RA	RA	Mizushima-Sugano J., Satoch T., Shirai Y., Takehashi Y., Nakagawa K.,		
RA	RA	Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,		
RA	RA	Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;		
RT	RT	"Complete sequencing and characterization of 21,243 full-length human cDNAs";		
RT	RT	EMBL: AY02179; AAC1591-1;		
RT	RT	EMBL: BC027966; AAH17966-1;		
DR	DR	EMBL: AK027642; BAB55258-1; -.		
DR	DR	KW		
DR	DR	Cell division.		
SQ	SQ	SEQUENCE 371 AA; 42573 MW; 30244E3057D9C43 CRC64;		
Alignment Scores:				
pred. No.:	4.6e-153	Length:	371	
score:	1929.00	Matches:	364	
Percent Similarity:	98.11%	Conservative:	0	
Best Local Similarity:	98.11%	Mismatches:	7	
Query Match:	98.32%	Indels:	0	
DB:	2	Gaps:	0	
US-10-046-935-2234 (1-1116) × Q9BW1 (1-371)				
Qy	1	ATGGACGCTCCGCCGTGCCAGAAGATCTAGAGTAAAGAACCTAAAGAAATT		
Db	1	MetAsPAlaAsArgValProGlnlySaspIeuArgVallySlysAsnleuLyblySphe		
Qy	61	AGATATGAACTGATTTCGAAACACAGGCTGACTGCTTCATCTGTGAGTGAAGTTGACAGCTGGCGAAGGCTGAGGCTGAGGAC		
Db	21	ArgTyVallySlysLeuIleSerNetGluThrSerSerSerAspSpSerCyAspSer		
Qy	121	TTTGCTCTGATAATTTCGAAACACAGGCTGACTGCTTCATCTGTGAGTGAAGTTGACAGCTGGCGAAGGCTGAGGCTGAGGAC		
Db	41	PheAlaSerAspAsnPheAlaAsnThrArgLeuGlnSerValArgLysGluGlyCysargIn		

Db	200	AlaLeuProThrGluGluGluGluGluGluGluAspLysTyrMetLeu	219		RT RN RP SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
Qy	622	GTCGAAGACGAACTCCGTGATGGTCACTGATGAAAGTGCCTGCCGCTGAGCTGCCAGAGCCGT	681		RC RA Strainsberg R.; Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
Db	220	ValArgGluArgLyssSerMetAspSerTyrMetAsnAspAspAspValProArgSerArg	239		RL DR EMBL: BC066169; AAH66169.1; DR InterPro: IPR00972; Cypredoxin.
Qy	682	CGCTCCAGATAATCGCATGATATAATTGCCCAGTGAAAGATAAACAGAG	741		RW Cell division: SQ SEQUENCE 382 AA: 43865 MW: C8920663588CCFF7 CRC64;
Db	240	ArgPro--GlySerMetLeuProHisLeuTyrProValGluGluValThrGlu	258		
Qy	742	GAGGACTGGAAACGCTCGAGCAATTCTCGAGAAAGATAATPACCGTCACTGGCC	801		Alignment Scores: Pred. No.: 3.15E-126 Length: 382 Score: 1609.50 Matches: 308 Percent Similarity: 86.72% Conservative: 25 Best Local Similarity: 80.21% MisMatches: 36 Query Match: 82.03% Indels: 15 DB: 2 Gaps: 5
Db	259	GlugluiIeargasnIecysSerIasnSerargGluIlysIetyAsnAgsSerIeuGly	278		US-10-046-935-2234 (1-1116) x Q6NZES (1-382)
Qy	802	TCTACTTGTGCTCATGCCCCATGAAAGACTTATGATCCAAACAGAGAAACCCA	861		Qy 1 ATGGAGCTCCGGAGAAACCTCGTATCCTCTGTGACAGCTGTGACAGC 60
Db	279	SerThrCysIisGlnCysArgInlysthrAspThrIysthrAsnCysArgAsnPro	298		Db 1 MetGluIalaArgGralAArgGlnlysAlaIeulysVal--LyAsnIeulysAspVal 19
Qy	862	GACTGCTGGGGCGTTCGAGGCAAGTCTGGCCCTGCTCTCGAACCTTATGGTGA	921		Qy 61 AGATATGTAAGGTTGATTTCATGGAAACCTCGTATCCTCTGTGACAGC 120
Db	299	AspCysTrpGlyIleArgGlyGlnPheCysLysProCysIeuArgTyrGlyGlu	318		Db 20 ArgtryMetylSLeuIeserMetGluIthrSerSerSerAspSerCysAspSer 39
Qy	922	GAGTCAGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	981		Qy 62 1 TTGGCTTCTGATAATTGCAAACAGGAGCTGCAGTCAGTGGAAAGCTGAGACC 180
Db	319	GluvAllYlysIspaIaleLeuAspProAsnTrpIscysPtoProCysAsgGlyIleCys	338		Db 40 PheAAspSerAspPheAAsnThrArgLeuGlnLeuAsnIrrArgGluGlyCysArgThr 59
Qy	982	AACCTGAGTTCTGCGGGCAGCGAGCTGGGAGCTGGGACTGGCTCTGGTATTAA	1041		Qy 181 CGCAGCAGTGCAGGCACTTGGA CCTCTGGGAGTTCAGGGCTCAGCGGGAGT 240
Db	339	AsnCysSerPheCysArgGlnArgAspGlyIargCysAlaThrGlyValLeuItyLeu	358		Db 60 ArgSerGlnCysArgIhsSerGlyProLeuArgYalaMetLysPheProAlaArgAsn 79
Qy	1042	GCCAAATATCTGGCTTGGGAATGTGCAATCCACTTGAAGGCTGAAACAGAAATT	1101		Qy 241 ACCAGGGAGGAAACCCAACAAAAAGCAGGAGTCCGCCTCAGAGAAATTCTGTGACT 300
Db	359	AlaIstsYtrIstsGlyPheGlyAspValHisIalatYlreLeuIstsSerIeuGlnGluPhe	378		Db 80 ThrArgGalaIalaSerIysAlaIalaProProLysProSerGluUserAlaAsn 99
Qy	1102	GAATGCAAGGA 1113			Qy 301 GATTCCAACCTCGATICA-----GAAGATGAAAGTGGAAATGGAAT 339
Db	379	GlumMetGlnAla 382			Db 100 AspSerHistAspSerIeuGluGluGluGluIlysGlyMetAsn 119
RESULT 4					
Q6NZES		PRELIMINARY; PRT; 382 AA.			Qy 340 TTITGGAGAAAGGCCCTTAATAATAAGGAAACATGCTGAAACATCTG 399
ID	Q6NZES				Db 120 PheLeuGluIysArgIalaLeuAsnIleLysGlnAsnLysAlaMetLeuAlaLysLeuMet 139
AC					Qy 400 TCTGAATTAGAAAGCTTCCCTGGCTGTTCCGGAGAGACATCCCTCCAGGCTCGAC 459
DT	05-JUL-2004	(T-EMBLrel. 27, Created)			Db 140 SerGluIeuGluUserDheProGlyLeuPhsSerGlyArgIhsSerIeuProGlyHisArg 159
DT	05-JUL-2004	(T-EMBLrel. 27, Last sequence update)			Qy 460 TCACAA---TCAAGGGAGGACCGCGAACGGPACATCCGGGATGTTCCAGGAAAC 516
DT	05-JUL-2004	(T-EMBLrel. 27, Last annotation update)			Db 160 AlaIysAspSerIysSerProArgArgIhrPhsProGlyvalAlaIlysArgAsn 179
DE		Cell division cycle associated 7.			RA 517 CCTGAAAGGAGGCTGCTCTTACAGGTCAAGGTCAGGATCTCGGTCCCTTGAC 576
GN		Name=Cdc4a;			RA 180 ProGluArgArgIhrArgProLeuIhrArgSerArgIleGlySerIeuGly 199
OS		Mus musculus (Mouse)			RA 577 GCTCTACCACTG-----GRGAGAGGCACTTGKARMTMWGTCATGTTG 621
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			Db 200 AlaLeuProThrGluGluGluGluGluGluGluAspLysTyrMetLeu 219
OC		Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus.			RA 622 GTGAGAAAGGAGGAAAGCCTGATGGCTCATGATGAAAGTGCCTGCCAGAGACCGT 681
OX		NCBI TaxID:10096;			RA 220 ValArgSerIysGlySerSerProArgArgSerArgIleGlySerAspAspIys 239
RN		[1]			RA 682 CGCTCCAGATCATCCGTCGACCTTCOGCATATAATTGCCCACTGGAAGAAATTACAGAG 741
RP		SEQUENCE FROM N.A.			RA 240 ArgPro--GlySerMetThrLeuProHistIleArgProValGluGluValThrGlu 258
RC		SEQUENCE=C57BL/6J; TISSUE=Unfertilized egg;			RT "Generation and initial analysis of more than 15,000 full-length human
RX		MEDLINE=2388257; PubMed=12477932;			
RA		Klausner R.D., Collins F.S., Wagner L., Shearnan C.M., Schuler G.D.,			
RA		Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA		Rosenblatt R.L., Fengold E.A., Grouse L.H., Derge J.G.,			
RA		Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,			
RA		Stapleton M., Soares M.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,			
RA		Brownstein M.J., Usdin T.B., Toshiyuki I.S., Carninci P., Prague C.,			
RA		Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,			
RA		Bosak S.A., McEvon P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA		Richards S., Worley K.C., Hile S., Garcia A.M., Guy L.J., Hulyk S.W.,			
RA		Villanova D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA		Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA		Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA		Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA		Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA		Krzywinski M.I., Skalska U., Smilius D.E., Schmerch A., Schain J.E.,			
RA		Jones S.J., Marrs M.A.,			
RT		"Generation and initial analysis of more than 15,000 full-length human			

QY	SEQUENCE	382 AA;	43865 MW;	C8920663588BCCF7 CRC64;
7442 GAGGAGTTGGAAAGCTGCGACATTCTGAGGAAGATATAACCGTTCACTGGC 801				
2539 GluGluIleArgAsnIleCysSerasnSerasnSerasnSerasnSerLeuGly 278				
8022 TCTACTTGTCATCATGCGCTTCAGAAGACTTATTGATAACCAAACAAACTGAGAACCCA 861				
279 SerThrCysHisGlnCysArgGlnLysThrAspThrlysThrAsnCysArgasnPro 298				
8632 GACTCTGGCGCGTTCGAGGCCAGTCTGNGCCCTTCGAAACCGTTATGGTCAA 921				
299 AspcystTrpGlyIleArgGlyInpheCysGlyProCysIleuArgAsnAlaGly 318				
922 GAGGTCAAGGATGGCTCTGCCTGCGATCCGAATGGCATTGCCGCGCCTGTCAGGAACTGC 981	QY			
3119 GluValLysAspAlaLeuIleAspProCysProCysArgGlyIleCys 338	Db			
982 AACTCGAGTTCTGCGGAGATGGAGCTGACTGGGCTCTCTGTGTGATTAA 1041	QY			
339 AsnCysSePheCysArginArgaspGlyArgCysAlaThrGlyValLeuValTyrLeu 358	Db			
1042 GCCAATATCATGGCTTTCGGAATGTGATGCTGACTTGAAGACGAAATT 1101	QY			
359 AlaArgTyrIleSglPheGlyAsnValHIsAlaTyrLeuIleSerLeuIleGluIle 378	Db			
1102 GAAATGCAAGCA 1113	QY			
379 GluMetGlnAla 382	Db			
RESULT 5				
AAH66169 PRELIMINARY; AAH66169 PRELIMINARY;	PT;	382 AA.		
DT 02-MAR-2004 (TRIMBirel. 27, Created)	DT 02-MAR-2004 (TRIMBirel. 27, Last sequence update)			
DT 02-MAR-2004 (TRIMBirel. 27, Last annotation update)	DT 02-MAR-2004 (TRIMBirel. 27, Last annotation update)			
Mus musculus (Mouse).				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1]				
SEQUENCE FROM N.A. STRAIN=57BL/6J; TISSUE=Unfertilized egg; MEDLINE=22388257; PubMed=12477932;				
straussberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Diatchenko L., Matsunaga K., Farmer A., Rubin G.M., Hong L., Stepanov M., Soares M.B., Ronald M.P., Cesavant T.L., Scheetz T.E., Brownstein M.J., Ustidin T.B., Toshiyuki S., Carninci P., Prange C., Raba S., Loquelineau N.A., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McEwan P.J., McErlean K.J., Malek J.A., Gunnarsson P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muniz D.M., Soderquist E.J., Lu X., Gibbs R.A., Fahay J., Helton F., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.B., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [2]				
SEQUENCE FROM N.A. STRAIN=57BL/6J; TISSUE=Unfertilized egg; straussberg R.; Submitted (PEB-2004) to the EMBL/GenBank/DBJ databases. EMBL; B006169; ARH66169.1; Cell division.				
Db Alignment Scores:	Pred. No. :	3.15e-126	Length:	382
Score:		1609.50	Matches:	308
Percent Similarity:		86.72%	Conservative:	25
Best Local Similarity:		80.21%	Mismatches:	36
Query Match:		82.03%	Indels:	15
DB:	Gaps:	2	Gaps:	5
US-10-046-935-2234 (1-1116) x AAH66169 (1-382)				
QY 1 ATGGAGCTGCCGCGCTGAGAATGCTCAGAGTAACGAACTAAAGAAATT 60	QY			
1 MetGluAlaArgAlaArgAlaArgClnlysAlaLeuIleLysVal--LysAsnLeuLysAspVal 19	Db			
61 AGATAGTGAGTTGATTCCATGGAAACCTCGTCATCTCTGATGACAGITGTGACAGC 120	QY			
20 ArgTyMethylsLeuIleSerMetGluThrSerSerSerAspSerCysAspSer 39	Db			
121 TTGGCTCTGATAATTGCAAACACGAGCTGCAAGTCGGAGGCTGTAGGAC 180	QY			
40 PheAlaSerAspAspPheAlaAsnThrArgLeuIleAsnThrArgLeuIle 59	Db			
181 CGCAAGCAGTCAGCTGAGGACTCTCGGACCTCTCGGGCTCCACCGCGAGT 240	QY			
60 ArgSerClnCysArgHsSerLysProLeuArgValAlaMetLysPheProAlaArgAsn 79	Db			
241 ACCAGGGAGGAAACCAAAAGAGAGTCGGCCTCTAGAAATCTGTGACT 300	QY			
80 ThrArgArgAlaAlaSerLysAlaAlaProproLysProSerGluSerAlaAsn 99	Db			
301 GATTCCAACCTCGATICA-----GAGATGAAAGTGCTGATGAACT 339	QY			
100 AspSerHsSerAspSerGluGluGluGluGluGluGluGluGlu 119	Db			
340 TTTTGAGAGAAAGGCGTTAAATATAAGCCAAAGGAACTATGTTGCAAACTGTATG 399	QY			
120 PheLeuGluysArgAlaLeuAsnIleysGlnAbuLysAlaMetLeuIalysLeuMet 139	Db			
400 TCTGAAATTGAAAGCTTCCTGGCTGCTCGTGGAGAGATCCCTCCAGGCTCGAC 459	QY			
140 SerGluLeuGluSerHerProGlyLeuPheSerGlyArgHsSerLeuProGlyHsArg 159	Db			
460 TCACAA----TCAAGGAGACCCGAGCCGCTACATCCGGCTGCTTCAGGAGAAC 516	QY			
160 AlaLysAspSerLysSerProArgArgArgThrProGlyValAlaThrArgAsn 179	Db			
517 CCTGAACTGGAGACGCTGCTCCGATTCAGGTCAGCTGGGCTCCPTGAC 576	QY			
180 ProGluArgArgGthArgProLeuThrArgSerArgSerArgIleGlySerLeuGly 199	Db			
577 GCTCTACCATG-----GRGAGAGCCAGTTTKGARAKTMNGTACATGTTG 621	QY			
200 AlaLeuProIleGluGluGluGluGluGluGluGluGluGluGlu 219	Db			
622 GTGAGAAAGAGGAAGACCGTGGATCATGATGAAAGTAGCTGCCAGAAAGCCGT 681	QY			
220 ValGlnGlnArgLysSerMetAspPaspPaspPaspPaspPaspPaspPasp 239	Db			
682 CGCTTCAGAGCATCCTGAGCATATANTCCTGAGAGATAATAACGGTCTCGGGC 801	QY			
240 ArgPro---GlySerMetThrLysLeuIleArgProValGluValThrGlu 258	Db			
742 GAGGGTTGGAGAAAGCTGAGGAGATAATAACGGTCTCGGGC 801	QY			
259 GluGluIleArgAlaCysSerAsnSerArgIleLysAsnArgSerIleLys 278	Db			
802 TCTACTTGTCATCATGCGCTCAGAGAATCTGAGAAACTGAGAAAACCA 861	QY			
279 SerThrCysHisGlnCysArgGlnLysThrAsnCysArgAsnPro 298	Db			
862 GACTGCTGGGGCGTGTGAGGCCAGTCTGTCGGCCCTGCCTGAGAACCGTTATGGTCAA 921	QY			

Db	299	A spcYstrpGlyIleargGlyIleGlyInPheCysGlyProCysLeuArgPsaG-TyrglyGlu	318
QY	922	GAGGTAGGGATGCTGTGATCGAACCTGCACTGGATTGCCGCCTGTCAGGAATCTGC	981
Db	319	GluvalylasparalayleaspProAsnTriPhicySProProysArgGlyIleCys	338
QY	982	AACTGCAGTTCTGCCGGACGGAGTGGACACTGGCTGTGCACTGGCTCCCTGTGTATTTA	1041
Db	339	AsnCysSerpCysArgGlnArgArgIgylargCysAlaIgylgylLeuValtryLeu	358
QY	1042	GCCAAATATCATGGCTTGGAAATGTCGOCATGCCTATTGAAAGCTGAAACAGGAAATT	1101
Db	359	AlaArgTyryHisGlyIgylgylAsnvalHisAlaTyryLeuLysSerIeulysglnGluPhe	378
QY	1102	GAAATCAAGA 1113	
Db	379	GluCeuGlnIala 382	
RESULT 6			
	Q8C1A0	PRELIMINARY;	PRT;
	ID Q8C1A0		382 AA.
	AC Q8C1A0;		
	DT 01-MAR-2003 [T=EMBL]	23; Created)	
	DT 01-MAR-2003 [TREMBL]	23; Last sequence update)	
	DT 01-JUN-2003 [TREMBL]	24; Last annotation update)	
	DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone 4732431F21 product similar to C-MYC TARGET JPO1 (CDNA Name=Cdcda7,		
	DE FLUJ4736 FIS, CLONE NT2RP302181).		
	GN OS	Mus musculus (Mouse).	
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	NCBI_TaxID=10050;		
	[1] RN	SEQUENCE FROM N.A.	
	RC STRAIN=C57BL/6J; TISSUE=Skin;		
	RX MEDLINE=92279233; PubMed=10349636;		
	RA Carninci P.; Hayashizaki Y.;		
	RA RT "High-efficiency full-length cdna cloning.";		
	RA Meth. Enzymol. 303:19-44(1999)."		
	[2] RN	SEQUENCE FROM N.A.	
	RC STRAIN=C57BL/6J; TISSUE=Skin;		
	RX MEDLINE=21085660; PubMed=11217851;		
	RA RIKEN FANTOM Consortium;		
	RA RT "Functional annotation of a full-length mouse cdna collection.";		
	RA Nature 409:685-690(2000).		
	[3] RN	SEQUENCE FROM N.A.	
	RC STRAIN=C57BL/6J; TISSUE=Skin;		
	RX MEDLINE=20499314; PubMed=110212159;		
	RA Carninci P.; Shibusawa Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.,		
	RA Konno H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;		
	RA "Normalization and subtraction of cap-trapper-selected cdnas to prepare full-length cdna libraries for rapid discovery of new genes.";		
	RA Genome Res. 10:1617-1630(2000).		
	[4] RN	SEQUENCE FROM N.A.	
	RC STRAIN=C57BL/6J; TISSUE=Skin;		
	RX MEDLINE=20530913; PubMed=1106861;		
	RA Shiblett K.; Ichih M.; Aizawa K.; Negaoaka S.; Sasaki N.; Carninci P.,		
	RA RA Konno H.; Akiyama J.; Nishi K.; Katsunai T.; Tashiro H.; Itoh M.,		
	RA RA Sumi N.; Ishii Y.; Nakamura M.; Harada A.; Nishina T.; Harada A.,		
	RA Yamanoto R.; Matsubimoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;		
	RA RA "Rapid construction of cap-trapper-selected cdnas to prepare full-length cdna libraries for rapid discovery of new genes.";		
	[5] RN	SEQUENCE FROM N.A.	
	RC STRAIN=C57BL/6J; TISSUE=Skin;		
	RX MEDLINE=20499314; PubMed=110212159;		
	RA Carninci P.; Shibusawa Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.,		
	RA Konno H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;		
	RA "Normalization and subtraction of cap-trapper-selected cdnas to prepare full-length cdna libraries for rapid discovery of new genes.";		
	RA Genome Res. 10:1617-1630(2000).		
	[6] RP	SEQUENCE FROM N.A.	
	RC STRAIN=C57BL/6J; TISSUE=Skin;		
	RX MEDLINE=20530913; PubMed=1106861;		
	RA Shiblett K.; Ichih M.; Aizawa K.; Negaoaka S.; Sasaki N.; Carninci P.,		
	RA RA Konno H.; Akiyama J.; Nishi K.; Katsunai T.; Tashiro H.; Itoh M.,		
	RA RA Sumi N.; Ishii Y.; Nakamura M.; Harada A.; Nishina T.; Harada A.,		
	RA Yamanoto R.; Matsubimoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;		
	RA RA "Rapid construction of cap-trapper-selected cdnas to prepare full-length cdna libraries for rapid discovery of new genes.";		

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.", Genome Res. 10:1757-1771 (2000). [6]
SEQUENCE FROM N.A.
P STRAIN=C5/B/L/60; TISSUE=Skin;
C Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kasukawa T., Kato H., Katoch H., Kawai J., Kojima Y., Kondo S., Konno H., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shitaki T., Sogabe Y., Togami M., Tagawa A., Takahashi F., Takaku-Akibira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted: JUL-2001; BAC26058.1.; EMBL: AK028671; BAC26058.1.; -.
R MGD: MGI:1914203; Ccdca7.
R Q SEQUENCE 382 AA; 43836 MW; 33F004EB500ED9EE CRC64;
B: Alignment Scores:
Scored No.: 4.64e-126 Length: 382
Score: 16.07±50 Matches: 309
Percent Similarity: 86.72% Conservative: 25
Best Local Similarity: 80.21% Mismatches: 36
Query Match: 81.93% Indels: 15
B: Gaps: 5
S-10-046-935-2234 (1-1116) x Q8C1A0 (1-382)
Y 1 ATGGAGCTCGCCGCGAGAAAGATTCAGAGTAAAGAGAACTTAAGAATTTC
b 1 MetGluAlaArgGalaArgInlySalaLeuLysVal--LysAsnLeuLysAspVal
Y 61 AGATATGTGAGTTGATTTCCATGGAAAACCTGTCTCATGCCATGAGCATGAGTCAGACGC
b 20 ArgTyMetylSLeuIleSerGluThrSerSerSerSerAspSerAspSer
Y 121 TTGCTTCTGATAATTTGCAAACACAGGGCTGCAGTCAGTCAGTGGGAAGGGCTGAGACC
b 40 PheAlaSerAspAsnHealaasnThrArgLeuIleAspArgGluGlycysArgThr
Y 181 CGACGCCAGTGAGGACTCTGACCTCTAGGGTGCAGTCAGTCAGGAGGT
b 60 ArgSerGlnCysArgHisSerGlyProLeuArgValAlaMetLysPheProAlaArgAsn
Y 241 ACAGGGGAGCAACCACAAAAAGCAGAGTCGCCAGCCCCAGAAATCTGTGACT
b 80 ThrAlaGargAlaAlserLysIaaAlaProProLysProSerAlaLysAlaAsn
Y 301 GATTCCAACCTCGATICA-----GAGATGAAAGTGGATGAT
b 100 AsnSerHissAspSerGluGluGluGluGluGluGluAspGlyMetAsn
Y 340 TTGTTGGAGAAAAGGCTTAAATAAAGAAACAAGCATGCCAGCTCCAGGCTCCGAC
b 120 PheLeuGluLysArgAlaLeuAsnIleLysGlnAsnLysAlaMetLeuAlaLysLeuMet
Y 400 TCTGAATTAGAAAGCTTCCTCTGGCTGGCTGGAGACATCCCCTCCAGGCTCCGAC
b 140 SerGluLeuGluSerPhePheProGlyIlePheserGlyArgHisArg
Y 460 TCACAA---TCAAGGAGACGCCGAGGGCTGACATTCCGGGTTGCTTCCGGAGAAC
b 160 AlalAspSerProArgArgArgArgArgArgArgArgAsn
Y 517 CCTGAAACGGAGAGGCTGCTTACAGGTAAGGTCCTGCGGATCTGGAC

US-10-046-935-2234 (1-1116) x Q9EBV8 (1-220)							
Db	180	ProglutArgGargThrArgProLeuThrArserArgileLeuGlyserLeuGly	199				
Qy	577	GCTTACCCATG-----GRGAGGCCAGTGTGKAROMTMGTACATGTTG	621				
Db	200	AlaLeuProThrGluGluGluGluGluGluGluAspLysTerMetLeu	219				
Qy	622	GTGAAAGGGAAACCGGGATGGTCATGAATGAAATGACTGCCCCAAGCGT	681				
Db	220	ValArgGlnArgLysSerMetAspSerTyrMetAspAspAspValProArgSerArg	239				
Qy	682	CGTCACCATGGGAGAGCCTTGCAATAATTGCCAGTGGAGAAATTACAGAG	741				
Db	240	ArgPro---GlySerMetThrLeuProLeuGluGluGluGlySerLeuGly	258				
Qy	742	GAGGAGTTGAGAAAGTCTGCAGCAATTCTGAGAACAGATATAACCGTTCACTGGCC	801				
Db	259	GluGluIleArgAsnIleCysSerAsnSerAsnSerAsnSerAsnSerLeuGly	278				
Qy	802	TCTACTTGTATCATGGCCAGAGACTATTGATACCAAAACAACTGAGAAACCA	861				
Db	279	SerThrCysHisGlnCysArgGlnLysThrAspThrLysThrAsnCysBArgAbnPro	298				
Qy	862	GACTCTGGCAATTCTCGAGAACGATATAACCGTTCACTGGCTACTGTGATCAA	921				
Db	299	AspCystPrgIleIeargGlyIglnPheCysBArgAsnArgIglnPheCysBArgIgln	318				
Qy	922	GAGGTAGGATGGCTCTGGATGGCATCGAACACTGGCATTCGCGGCCCTGTCAGGAATCTGC	981				
Db	319	GluValLysAspAlaLeuLeuLysAspProAsnThrPhisCysProCysLeuGlyIleCys	338				
Qy	982	AACCTGAGATGTTCTGGGGGAGGAGATGGCACTGGCTCTCTGTGATTA	1041				
Db	339	AsnCysSerPheCysArgGlnArgGlyIglnArgCysAlaThrGlyValLeuValTyrLeu	358				
Qy	1042	GCCAATATCATGGCTTTGGAAATGTCATGCTGAAAGCTGCTGAAACAGGAATT	1101				
Db	359	AlaLysTrhIleGlyIglnPheGlyAsnValHisAlaItyLeuLysSerLeuLysGlnGluPhe	378				
Qy	1102	GAATGCCAGGA 1113					
Db	379	GluMetGlnAla 382					
RESULT 7							
Q9EBV8	Q9EBV8;	PRELIMINARY;	PRT;	220 AA.			
AC	Q9EBV8;						
DT	01-DEC-2001	(TREMBLrel. 19, Created)					
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)					
DE	Hypothetical protein (Fragment).						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
NCBI_TaxID	9606;						
RN	[1]						
RP	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.						
DR	InterPro: IPR008972; Cupredoxin.						
RA	Strasbourg R.; Strasbourg R.; TISSUE=Kidney;						
RA	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.						
RA	InterPro: BC015124; ANH15124.1; -						
KW	Hypothetical protein.						
FT	NON_TER 1						
SQ	SEQUENCE 220 AA; 25570 MW; C0760EE9AB3899CB CRC64;						
Alignment Scores:							
Pred. No.:	4.07e-88	Length:	220				
Score:	1155.00	Matches:	212				
Percent Similarity:	96.80%	Conservative:	0				
Best Local Similarity:	96.80%	Mismatches:	7				
Query Match:	58.87%	Indels:	0				
Gaps:	2	Gaps:	0				
Pred. No.:	3.92e-57	Length:	207				
Score:	786.00	Matches:	155				

Percent Similarity:	99.36%	Conservative:	0	RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
Best Local Similarity:	99.16%	Mismatches:	1	RT	
Query Match:	40.06%	Indels:	0	RI	
DB:	2	Gaps:	0	RN	[2]
US-10-046-935-2234 (1-1116) × Q8NBY9 (1-207)		SEQUENCE FROM N.A.			
Qy	1 ATGGACGCTGCCCGTGGCCAGAAAGATCTCAGAGTAAGAGAACTTAAGAAATTTC 60	RC TISSUE-Eye;			
Db	1 MetAspAlaArgValProGlnLysAspLeuIleLysIleSph 20	SEQUENCE FROM N.A.			
Qy	61 AGATATGTAAGTTGATTTCATCGAAACCTCGCATCTCTGATGACAGTGTGACGC 120	Strausberg R.;			
Db	21 ArgTyrValLysIleLeuSerMetGluThrSerSerAspSerAspSerAspSer 40	Submitted (ISBP-2001) to the EMBL/GenBank/DDBJ databases.			
Qy	121 TTGGCTTCCTGATATTTCGAAACAGGCTCGAGTAGGGCTAGGGCTAGAAC 180	RA EMBL; BC014530; AAH14530.2; -.			
Db	41 PheAlaSerAspAsnPheAlaAlaThrArgLeuGlnSerValArgGluGlycysArgThr 60	NON-TER 1			
Qy	181 CGGAGCCAGTGGCAGGCACTCTGACCTCTCAGGTGGCATGAGTTTCAGGGAGT 240	SEQUENCE 442 AA; 50745 MW; C57A871694B2C4FD CRC64;			
Db	61 ArgSerGlnCysArgHisSerGlyProLeuIleGluAlaMetIleSphProAlaArgSer 80	Alignment Scores:	3.4e-54	Length:	442
Qy	241 ACCAGGGAGCACCAAAAGAGAGATGAAAGTGTGAAATTCTGTGACT 300	Pred. No.:	Score: 752.00	Matches:	172
Db	81 ThrArgGlyAlaThrAsnLysSphAlaGluSerArgGlnProSerGluAsnSerValThr 100	Percent Similarity:	57.36%	Conservative:	50
Qy	301 GATTTCAAACCTCCATTCTGAAAGTGAAGTGTGAAATTCTGTGACT 360	Best Local Similarity:	44.44%	Mismatches:	111
Db	101 AspSerAsnSerAspSerGluAspGluSerGlyMetAsnPhenLeuGluSargAlaLeu 120	Query Match:	38.33%	Indels:	54
Qy	361 AATATAAAGCAAAACAAGCAATGCTGCAAAACTCATGTCGAATTAGAAAGCTCCCT 420	DB:	2	Gaps:	10
Db	121 AsnIleLeuGlnAsnLysAlaMetLeuAlaLysLeuMetSerGluLeuGluSerPro 140	US-10-046-935-2234 (1-1116) × Q96C70 (1-442)			
Qy	421 GGCTCGTTCCGTGGTGAAGCATCCCTCCAGGTCCGACTCACATCA 468	Qy 22 CAGAAAGATCTCAGTAAGAAAGAGAACTTAAAGAAATTCAGATATGTAAGTGATTTC 81			
Db	141 GlySerPheArgLysArgHisProLeuProGlySerAspSerValSer 156	Db 77 GluSerAspLeuAsnGlyLysThrAspProGlu-----VaMet 89			
Qy	9	Db 82 ATGGAAACCTCTCATCTCTGATGACAGGTTGACAGCTTGTGATTAATTTCGA 141			
Db	Qy 90 ValValGluUserAspLeuUserAspGlyLysAlaSerLeuValSerGluGluGlu 109	Qy 90 ValValGluUserAspLeuUserAspGlyLysAlaSerLeuValSerGluGluGlu 109			
Qy	101 AACACGAGGTGCGACTGAGTTGCGGAAGGGCTGTAGGCCGAGCCGAGGGCACTCT 201	Db 142 AACACGAGGTGCGACTGAGTTGCGGAAGGGCTGTAGGCCGAGCCGAGGGCACTCT 201			
Db	110 AspGluGlu----GluAspLysAlaThrProArgArgSerGlySerGlySer 127	Db 110 AspGluGlu----GluAspLysAlaThrProArgArgSerGlySerGlySer 127			
Qy	202 GGACCTCTCAGGGGGATGAGTTTCAGGGGGATACCAGGGAGCACCAACAA 261	Qy 202 GGACCTCTCAGGGGGATGAGTTTCAGGGGGATACCAGGGAGCACCAACAA 261			
Db	128 IleGlyLeuArgValAlaPheGlnPheProThrLysSerLeuAlaAlaLysProAspLys 147	Db 128 IleGlyLeuArgValAlaPheGlnPheProThrLysSerLeuAlaAlaLysProAspLys 147			
Qy	262 AAAGCAGAGTCCCAGCCAG-----279	Qy 262 AAAGCAGAGTCCCAGCCAG-----279			
Db	148 AsnSerSerSerGluGlnLeuPheSerSerAlaArgLeuGlnAsnGluLysIleSer 167	Db 148 AsnSerSerSerGluGlnLeuPheSerSerAlaArgLeuGlnAsnGluLysIleSer 167			
Qy	280 -----	Qy 280 -----			
Db	168 LeuGluArgLysLysAspCysArgGlnValLeuGlnArgGluAspSerSerGluSer 187	Db 168 LeuGluArgLysLysAspCysArgGlnValLeuGlnArgGluAspSerSerGluSer 187			
Qy	307 AACCTCCGATTCTGAAAGTGTGAAGT-----GGAATGATTCTGGAGAAAAGGGCTTA 360	Db 188 GluAspProSerArgAspGluSerGlnGluSerSerAspAlaLeuLeuLysGlnGluMet 207			
Db	361 AATATAAAGCAAAACAAGCAATGCTGCAAAACTCATGTCGAATTAGAAAGCTCCCT 420	Qy 361 AATATAAAGCAAAACAAGCAATGCTGCAAAACTCATGTCGAATTAGAAAGCTCCCT 420			
Db	208 AsnIleLeuGlnAsnLysAlaMetLeuAlaLysLeuMetSerGluLeuGluSer 227	Db 208 AsnIleLeuGlnAsnLysAlaMetLeuAlaLysLeuMetSerGluLeuGluSer 227			
Qy	421 GGCTCGTTCCGTGGTGAAGCATCCCTCCAGGTCCGACTCACATCA 468	Qy 421 GGCTCGTTCCGTGGTGAAGCATCCCTCCAGGTCCGACTCACATCA 468			
Db	228 AspPheSerProValArg-----ThrProThrSerAspLysSerThrValArg 245	Db 228 AspPheSerProValArg-----ThrProThrSerAspLysSerThrValArg 245			
Qy	481 AGCGGTCATTCCTGGCTGCTTCAGGGA---AACCTGAAAGGAGGCTCTCT 537	Qy 481 AGCGGTCATTCCTGGCTGCTTCAGGGA---AACCTGAAAGGAGGCTCTCT 537			
Db	246 ArgAlaPheSerGluGlyGlnLeuThrArgGluArgMetAsnProThrArgSerAlaArgPro 265	Db 246 ArgAlaPheSerGluGlyGlnLeuThrArgGluArgMetAsnProThrArgSerAlaArgPro 265			
Qy	538 CTTACCAAGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGAGGCC 597	Qy 538 CTTACCAAGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGAGGCC 597			
Db	266 ProGluLysPhe-----AlaLeuGluAsnPheThrValSerAlaAla 279	Db 266 ProGluLysPhe-----AlaLeuGluAsnPheThrValSerAlaAla 279			
Qy	598 AGTTTKGARKTMWGTACATGTTGGTGGAGAACCCGTTGCTTACGTGAAT 657	Qy 598 AGTTTKGARKTMWGTACATGTTGGTGGAGAACCCGTTGCTTACGTGAAT 657			
Db	280 LysPheAlaLysGluLysPheArgArgLysSerThrIleGlyLysCysArg 299	Db 280 LysPheAlaLysGluLysPheArgArgLysSerThrIleGlyLysCysArg 299			
Qy	658 GAAGATGACCTGCCAGAACGGCTCCAGATCATCCGTGACCTTCGGCATATAART 717	Qy 658 GAAGATGACCTGCCAGAACGGCTCCAGATCATCCGTGACCTTCGGCATATAART 717			
Db	300 Glu-----TyrArgArgArgHisArgIleSer-----SerPhe 310	Db 300 Glu-----TyrArgArgArgHisArgIleSer-----SerPhe 310			

		Query Match:	38.33%	Indels:	54
		DB:	2	Gaps:	10
Db	342 IysIleTyrAspIysValLeuGlyAsnThrCysHisGlnLystrileAsp	361			
Qy	838 ACCAACAATGCAAACCCAGATGCTGGCCCTCGGCCAGTTGTGCC 897				
Db	362 ThrLysThrValCysAgaAsnGlnGlyCysGlyvalArgGlyinPheCysGlyPro	381			
Qy	898 TGCCTTGAAACGTTATGGTGAAGAGTCAGGATCTCGATCCGAAACTGGCAT 957				
Db	382 CysLeuArgAsnArgTyrGlyIysAspValAspSerIleLeuAspPraAspIysPra	401			
Qy	958 TGCCCGCTTGCTGAGGAATCTGCAACTGAGCTTCGCCAGGAGATGGACCTGT 1017				
Db	402 CysProProCysArgGlyIleCysAsnCysSerTyrCysArgAspGlyArgCys	421			
Qy	1018 CGGACMGCGGNCCTTGCTGTAATTAGCCAAATATCAGCGCTTGGGATGTCATGCTAC 1077				
Db	422 AlaThrClyIleLeuIleHisIeuAlaLysPheTyrGlyTyraspAsnValLysGluTyr	441			
Qy	1078 TTGAAAGCCTGAAACCGAA 1098				
Db	442 LeuGluSerIeuGlnIysGlu 448				
RESULT 11					
ID AAH25242	PRELIMINARY;	PRT;	453 AA.		
AC AAH25242;					
DT 29-MAR-2004 (TMBMLrel. 27, Created)					
DT 29-MAR-2004 (TMBMLrel. 27, Last sequence update)					
DT 29-MAR-2004 (TMBMLrel. 27, Last annotation update)					
DE Transcription factor RAM2.					
GN RAM2.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX NCBI_Taxid:9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Eye;					
RX MEDLINE=22388257; PubMed=12477332;					
RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA Altenschl S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,					
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,					
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prage C.,					
RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahay S.J.,					
RA Bosak S.A., McEvany P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA Richards S., Worley K.C., Hale S., Garcia A.M., Guy L.J., Hulyk S.W.,					
RA Villaon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,					
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Buffard G.G.,					
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,					
RA Krzywinski M.I., Skalska U., Smailus D.E., Schenck J.E.,					
RA Jones S.J., Marra M.A.;					
RT "Generation and initial analysis of more than 15,000 full-length human					
RT and mouse cDNA sequences.";					
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).					
RN [2]					
RP SEQUENCE FROM N.A.					
RC TISSUE-Eye;					
RA Straubberg R.i.					
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.					
DR EMBL: BC025242; AAH25242.; -					
SQ SEQUENCE 453 AA; 52078 MW;	4C7B2BF1134CFB74 CRC64;				
Alignment Scores:					
Pred. No.:	3.42E-54				
Score:	752.00	Length:	453		
Percent Similarity:	57.36%	Matches:	172		
Best Local Similarity:	44.44%	Conservative:	50		
		Mismatches:	111		

BLANK

PS Claim 2; SEQ ID NO 2235; 105pp; English.
 XX ABL36412 fo ABL38645 represent human colon tumour antigen cDNA clones (1)
 CC which were isolated from human colon tumour and colon metastatic tumour
 CC cDNA libraries. (1) have cytostatic activity and can be used in vaccine
 CC production. (1) can be used for stimulating and/or expanding T cells
 CC specific for a tumour protein on contact with the T cells. They are also
 CC useful for inhibiting the development of cancer in a patient. (1) can be
 CC used as probes or primers for nucleic acid hybridisation, for preparing
 CC mutant species primers, or primers for use in genetic constructions. (1)
 CC can be used in the diagnosis of a colon tumour. The present sequence
 CC represents a human colon tumour antigen amino acid sequence which is
 XX specifically claimed in the present invention

Sequence 371 AA:

Alignment Scores:
 Pred. No.: 6.07e-196 Length: 371
 Score: 1943.00 Matches: 371
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Minmatches: 0
 Query Match: 99.03% Indels: 0
 Db: 5 Gaps: 0

US-10-046-935-2234 (1-1116) x ABB05376 (1-371)

Qy 1 ATCGACGCTGCCGGTGGAAAGATCTCAGATAAGAGAACCTAAAGAATTTC 60
 Db 1 MetAspAlaArgPheGlyValProGlnLysAspLeuArgValLysSerLeuIleuLysPhe 20

Db 21 ArgTyryValLysLeuIleuSerMetGluThrSerSerSerAspAspSerGlyAspSer 40
 Qy 61 AGATATGTGAAGTGATTCCATGGAAACCTCGTCATCCTCTGATGAGCTGAGGC 120
 Db 21 ArgTyryValLysLeuIleuSerMetGluThrSerSerSerAspAspSerGlyAspSer 40

Qy 121 TTGCTCTGTGATAATTTCGAAACAGGGGGCTCAGTCAGTTGGAGGGCTGTAGACC 180
 Db 41 PheAlaSerAspAsnPhaaAlaAsnThrArgLeuLysSerValArgGluGlyLysAspThr 60

Qy 181 CGAGCCAGTCAGGGCATCTGACACTTCAGGGTGGCATGAGTTCCAGCGGAGT 240
 Db 61 ArgSerGlnGlySarGlySerGlyProLeuArgValAlaMetLysPheProLaaArgSer 80

Qy 241 ACCAGGGGAGCAACCAACAAAAGCAGATCCGCGCCCTCAGAACATTCTGTCAT 300
 Db 81 ThrArgGlyAlaThrAsnLysLeuLysSerAspLysSerArgInProGlnProSerValThr 100

Db 82 PD 07-FEB-2001.
 Qy 301 GATTCCAACCTCGATTCTAGAAAGATGAAAGTGGAAATGAAATTTTGGAGAAAGGGCTTA 360
 Db 101 AspSerAsnSerAspSerGluLysSerGlyMetAsnPheLeuGluLysArgAlaLeu 120

Qy 361 AATAAAACAAACAAGCAAAAGCTTCAAACTCATGTCGAATTAGAAAGCTTCCCT 420
 Db 121 AsnLysLeuLysLeuLysLeuMetSerGluLysLeuSerPhePro 140

Qy 421 GGCGCGTTCGTTGGAAAGACATCCCTCCAGGGTCCGACTCAAACTAGGAGACCGGA 480
 Db 141 GlySerPheArgGlyArgGlyProLeuProGlySerAspSerSerArgGlyProArg 160

Qy 481 AGCGGTACATTCCGGGTTGGCTTCAGGAGAAACCTGAACGGAGAGCTCGTCCT 540
 Db 161 ArgarginPheProGlyValAlaSerGlySerAsnProGluLysArgProLeu 180

Qy 541 ACCAGGTCAAGGTCGGGATCCGGGTTGGCTTCAGGAGAAACCTGAACGGAGCT 600
 Db 181 ThrArgSerArgSerArgSerArgSerArgSerArgSerAspSerLeuAspAlaLeuPromet**ArgAlaSer 200

Qy 601 TTGKARNMWPACATGTTGGTAGAAAGAGAAACCTGAACGGAGCTCGTCCT 660
 Db 201 **Glu*****TyrMetLeuValArgLysArgLysSerValThrLeuProHisIleLysArg 240

Qy 661 GATGACCTGCCAGAAGCCGTCGCTCAAGATCATCCGTGACCCCTTCCCCTATAATTTCGC 720
 Db 221 AspAspLeuProArgSerArgSerArgSerValThrLeuProHisIleLysArg 240

Qy 721 CGGTGGAGAAATAAGAGGGAGTTGGAGAACCTCTGAGCAATTCTGAGAGAAG 780
 Db 241 ProValGluGluIleThrGluGluLeuGluAsnValCysSerAsnSerArgGlnLys 260
 Qy 781 ATATATAACCGTTCACTGGGCTCTACTTGTCAATGCGCTCAGAAAGACTATTGATACC 840
 Db 261 IleTerTyrAsnTerGlySerLeuGlySerGlySerGlySerGlySerGlySerGly 280
 Qy 841 AAAACAAACTGAGAACCCAGACTGTGGGGCGCTTGAGGGCAAGCTCTGCGCCCTG 900
 Db 281 LysTerAsnCysArgAsnProAspCysTrpGlyValArgGlyGlnPheCysGlyProCys 300
 Qy 901 CTCGAAACCGTTATGTGAAGAGTCAGGATGCTGCTGAGATCCGAACCTGGCATTCG 960
 Db 301 LeuArgAsnArgTyrGlyGluLysLeuAspAspAlaLeuLeuAspProAsnTrpHisCys 320
 Qy 961 CCCGCTTCTGAGGAATCTGCAACTGCAACTGCAAGTTCTGCGGAGATGGACCGTGTGCG 1020
 Db 321 ProProCysArgGlyLysCysSerPheCysSerGlyLysArgAspGlyArgCysAla 340
 Qy 1021 ACTGGGTCCTCTGTGTATTAGCTCAATATCATGGCTTTGGGAAATGTGCATCCCTACTTG 1080
 Db 341 ThreGlyValLeuValTyrLysLeuLysTyrHsGlyTheGlyAsnValHisAlaTyrLeu 360
 Qy 1081 AAAAGCTGTAACAGGATTGAAATGCAAGA 1113
 Db 361 LysSerLeuLysGlnGluPheGluMetGlnAla 371

RESULT 2
 AAB94473
 ID AAB94473 standard; protein; 371 AA.
 XX AAB94473;
 XX DT 26-JUN-2001 (first entry)
 XX DE Human protein sequence SEQ ID NO:15139.
 XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX OS Homo sapiens.
 XX PN EP1074617-A2.
 XX PN EP1074617-A2.
 XX PD 07-FEB-2001.
 XX XX 28-JUL-2000; 2000EP-00116126.
 XX PR 29-JUL-1999; 99JP-00248036.
 XX PR 27-AUG-1999; 99JP-0030053.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 03-JUN-2000; 2000JP-00241899.
 XX PA (HELI-) HELIX RES INST.
 XX PA (HELI-) HELIX RES INST.
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX Claim 8; SEQ ID NO 15139; 2537pp + Sequence listing; English.

CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-DT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602

nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAI03166 to AAI13628 and AAI13633 to AAI13642 represent human cDNA sequences; AAB92446 to AAB9893 represent human amino acid sequences; and AAI13629 to AAI13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence 371 AA;

Alignment Scores:
 Pred. No.: 1. 1.84e-194
 Score: 1.929.00
 Percent Similarity: 98.11%
 Best Local Similarity: 98.11%
 Query Match: 98.32%
 DB: 4 Gaps: 0

US-10-046-935-2234 (1-1116) × AAB94473 (1-371)

Qy 1 ATGGACGCTCGCGCGNGCCGGAGAAAGATCTCAGACTAAAGAAACTTAAAGAAATTTC 60
 Db 1 MetAspAlaArgValProGlnLysAspLeuArgValLysLeuLysSph 20
 Qy 61 AGATATGTGAAGTTGATTTCATGGAAACCTCTGATCACCTCTGATGACAGTTGTGACAGC 120
 Db 21 ArgTyrValLysLeuIleSerMetGluThrSerSerSerAspSerAspSer 40
 Qy 121 TTTCGCTCTGATAATTTCGAAACACAGGCTGCACTTGAGCTTCCAGGCTGTAGCGACC 180
 Db 41 PheAlaSerAspSerAsnAlaSerThrArgLeuInsSerArgLysSerArgThr 60
 Qy 181 CGCAGCCAGTGCAAGGCACCTCTGACACTCTCAGGTGGCGATCAAAGTTTCCAGGCCAGT 240
 Db 61 ArgSerGlnCysArgHisSerGlyProLeuArgValAlaMetLysSerProAlaArgSer 80
 Qy 241 ACCGGGGAGCACCAAAAGCGAGTCGGCCAGCTCTAGAGAAATCTGAGACT 300
 Db 81 ThrArgGlyAlaThrAsnLysAlaGluUserArgGinProSerGluAsnSerVaThr 100
 Qy 301 GATTCGCAACTCGGATTCAAGAATGAAAGTGGAAATGATGTTTGGAAAGAAAGGGCTTA 360
 Db 101 AspSerAsnSerAspSerGluAspGlyUserGlyMetAsnPhoLeuGluLysSerGlu 120
 Qy 361 AATATAAACCAAACAAAGCAATGCTGCAAATAACTCATGTCGAAATTAGAAAGCTTCCT 420
 Db 121 AsnLeuLysGlnAsnLysAlaLeuLeuLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeu 140
 Qy 421 GGCTCGTGTCCGTCGAGACATCCCCTCCAGACTCCACTCAAGAGAACCGCGA 480
 Db 141 GlySerPheArgLysArgHisProLeuProGlySerAspSerGlnSerArgProArg 160
 Qy 481 AGCGTAAATCCGGGTGTGGTCCAGGAGAACCTGAGCAGGAGCTGTCCTCTT 540
 Db 161 ArgArgThrPheProGlyValAlaSerArgGlnProGluLargGlnArgProLeu 180
 Qy 541 ACCAGGTCAAGTCGGCGATCTGGGTCGAACTGGCTGACGCTCTACCATGGRAGAGCCAGT 600
 Db 181 ThrArgSerArgSerGlySerGluAlaLeuProMetGluLgluGlu 200
 Qy 601 TTKGARKMTMMGWTACATGTTGGTAGAGAGAGAACGGTSGATGCTAATGATGAA 660

Db	201 GluGluAspLysTyrMetLeuValArgLysArgLysThrValAspGlyTyrMetAspGlu	220
Qy	661 GATGACCTGCCAGANGCCGNGCGCTGAGATCATCCGACGCTTCCGCATATAATCGC	720
Db	221 AspAspIeuProArgSerArgArgSerSerValThrLeuProHisLeuIleArg	240
Qy	721 CCAGTGCAGAGAAATTAGAGAGGGGTTGGAGAACCTCTGAGCAATTCTGAGAAAG	780
Db	241 ProValGluIleIleThrGluGluIleLeuGluAspValCysSerSerSerArgGlyLys	260
Qy	781 ATATATACCGTTTCACTGGCTACTCTGTCATCAATGCGCTCAGAGACTTGTGATC	840
Db	261 IleTerPheAsnGlySerLeuGlySerThiCysHsGlnLysSthrIleAspThr	280
Qy	841 AAAACACPAACTGCAGAACCCAGACTGTGGGGCGTGGGAGTGGCTGAACTGGCATTG	900
Db	281 LysThrAsnCysArgSerProSpCysTrpGlyValArgGlyGlnPheCysLysProCys	300
Qy	901 CTTCGAAACCGTTATGGTGAAGAGGTCAAGGATGGCTCTGGCATCCGAACTGGCATTG	960
Db	301 LeuArgAsnAspTyrGlyLysGluValArgAspAlaLeuLeuAspProAsnTrpHsCys	320
Qy	961 CGGCGCTTGCTGGAAATCTGCAACTGGAGTTCTGGGGAGCGAGATGGAAGGTGRCG	1020
Db	321 ProProCysArgLysLysCysAsnCysSerPheCysArgGlnArgGlyLysArgCys	340
Qy	1021 ACTGGGGTCCCTGTTGTTATTCATGGCTTTGGGAAATGCACTGCTACTTGT	1080
Db	341 ThreonineValValValValValValValValValValValValValValValVal	360
Qy	1081 AAAAGCTGAAACGGATTGAAACGGATTGAAATGAAATGCAAGGA 1113	
Db	361 LysSerIeuLysGlnGluPheGluMetGlnAla	
RESULT 3		
ABU56524	ABU56524 standard; protein; 371 AA.	
XX	ABU56524	
AC	ABU56524;	
XX	DT 02-APR-2003 (first entry)	
XX	DE Lung cancer-associated polypeptide #217.	
XX	KW Lung cancer-associated polypeptide; cytostatic; emphysema;	
XX	KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;	
XX	KW chronic obstructive pulmonary disease; benign lesion; bronchitis;	
XX	KW hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis	
OS	Unidentified.	
XX	PN WO200286443-A2.	
XX	PD 31-OCT-2002.	
XX	PF 18-APP-2002; 2002WO-US012476.	
XX	PR 18-APR-2001; 2001US-0284770P.	
PR 10-MAY-2001; 2001US-0290492P.		
PR 09-NOV-2001; 2001US-0339245P.		
PR 13-NOV-2001; 2001US-0350664P.		
PR 29-NOV-2001; 2001US-0334310P.		
PR 12-APP-2002; 2002US-0372246P.		
XX	(BOSB-) EOS BIOTECHNOLOGY INC.	
XX	Aziz N, Murray R;	
XX	WPI 2003-093161/08.	
DR N-PSDB; ABK76353.		
XX	Detecting a lung cancer-associated transcript in a cell from a patient	

PT for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.

PT XX Claim 27; Page 353; 453pp; English.

CC The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence that is at least 80% identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g., atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hyperactivity pneumonitis, interstitial pulmonary fibrosis, asthma, and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56498-ABU56745 represent lung cancer-associated polypeptides of the invention.

XX Sequence 371 AA;

Alignment Scores:
Pred. No.: 1.84e-194 Length: 371
Score: 1929.00 Matches: 364
Percent Similarity: 98.11% Conservative: 0
Best Local Similarity: 98.11% Mismatches: 7
Query Match: 98.32% Indels: 0
DE: 6 Gaps: 0

US-10-046-935-2234 (1-1116) x ABU56624 (1-371)

Qy 1 ATGGACGGCTGCCGCGTACCGCGAAAGAAATCTAGAGTAAGAGAACCTTAAGAANTC 60
Db 1 MetAspAlaArgArgValProGlnLysAspLeuArgValLysAsnLeuLysLysPhe 20

Db 21 ArgTyrrValLysIleIleSerMetGluThrSerSerSerAspAspSerCysAspSer 40

Qy 61 AGATATGTGAAGTTGATTTCATSGAACCTCTGAGCTCATCTCTGATGACAGTTGTGAGTC 120
Db 41 PheIleAspAspAsnPheAlaAnthrArgLeuGlnSerValArgIleGlycSarThr 60

Qy 181 CGCGGCCACTGGGCACTCTGACCTCTGACGGCTCAGTGTTGGGAAAGGTCTAGGACC 180
Db 61 ArgSerGlnCysArgHisSerGlyProLeuArgValAlaMetLysPheProAlaArgSer 80

Qy 241 ACCAGGGGAGCACCAAACAAAAGCAAGTCGGCCAGCTCAGAAATTGTGTGACT 300
Db 81 ThrArgGlyAlaThrAspLysValAlaGluSerArgGlnProSerGluAsnSerValThr 100

Qy 301 GATTCCTAATCCGATTCTGAGAAGATGGAATGAAATTGTTGGAGAAAGGGCTTTA 360
Db 101 AspSerAsnSerAspSerGluAspGluSerGlyMetAspHeLeuGluSerGly 120

Qy 361 AATATAAAGCAAAACAAGCAAAAGCTCAGAAACTCTGTCGAATAGAAAGCTTCCT 420
Db 121 AsnIleLysGlnAlaLysAlaMetLeuAlaLysLeuMetSerGluLeuSerPhePro 140

Qy 421 GGCTCGTCCGTTGGAGAGCATCCCTCCAGGTCTCGGACTCACATCAGGACCCGGA 480
Db 141 GlySerPheArgGlyArgHisProLeuProGlySerAspSerGlnSerArgArgProArg 160

Qy 481 AGGGGTACATTCCCGGTTGTTCCAGGAGAACCCGAAACGGAGAGCTCTCCRTTT 540
Db 161 ArgArgThrPheProGlyValAlaSerArgGlnProGluArgGalaArgProLeu 180

PT	QY	541 ACCAGGGTCAAGGTCCCGATCCCTGGGTCCTGACCTCATGRRGAGAGCCAGT 600
PT	DB	181 ThioArgSerArgIleArgLeuSerAlaLeuProMetGluGluGlu 200
PS	QY	601 TTGKARKMTMNGTACATGTTGGTGGAGACCCGTTGGCTCATGAAATGAA 660
PS	DB	201 GluGluAspLysTyrMetLeuValArgLysSarGlySarValAspGlyTyrMetAspGlu 220
CC	QY	661 GATGACCTGGCCAGAAGCCGCTCAGATCATCGTGAACCTTCGATGCG 720
CC	DB	221 AspAspIleProArgSerArgSerArgSerArgSerValThrLeuProHistidineLeuArg 240
CC	QY	721 CCAGTGAAGAAATACAGAGGAGTTGGAGAACCTGAGCATTCTGAGAGAG 780
CC	DB	241 ProValGluGluIleThrGluGluIleGluAsnValCysSerAsnSerArgIleIys 260
CC	QY	781 ATATATAACCCTGTTCACTGGGCTCTACTTGTCTATCATTGCTCAGAGACTATTGATACC 840
CC	DB	261 IleTerTyrAsnArgSerIleGlySerThrCysBisGlnGlySarGlnIysThrIleAspThr 280
CC	QY	841 AAAACAAACTGCGAAACCCAGACTGTGGCCGTTGAGGCAGTTGTCGCCCCTGC 900
CC	DB	281 LysThrIscNlysCysArgAsnProLysCysPheTrpGlyIvaArgGlyGlnPheCysGlyProCys 300
CC	QY	901 CTCGAAACCGTTATGGTAAAGCTAGGGATGCTGCTGATCGAACTGGCATGTC 960
CC	DB	301 LeuArgAsnArgTrpGlyGluValArgAspAlaLeuLeuAspProAsnIlePheIleCys 320
CC	QY	961 CCCCTGTTGAGGAATGTGCAACTGAGTTCTGGCGGACCGAGATGACCGTGTGCG 1.0/2
CC	DB	321 ProProCysArgGlyIleCysAsnCysSerPheCysArgGlnArgAspGlyIleCys 340
CC	QY	1021 ACTGGGCTCTCTGTATTAGCCAAATATCATGGCTTGGAAATGPGCATGCTACTTG 1080
CC	DB	341 ThreGlyValLeuItyLeuAlaLysThrIleGlyAsnValHisAlaTyIleu 360
XX	QY	1081 AAAAGGCCCTGAAACAGGAATTGAAATGCAAGGA 1113
XX	DB	361 LysSerLeuLysIleGluPheGluMetGlnAla 371
RESULT 4		
ID	ADF76612	standard; protein; 371 AA.
XX	XX	ACD F76612;
DT	DT	26-FEB-2004 (first entry)
DE	DE	Novel human secreted and transmembrane protein SeqID_286.
XX	XX	human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytosolic; chondrocyte; tumour.
XX	XX	Homo sapiens.
XX	XX	WO2003072035-A2.
PD	PD	04-SEP-2003.
XX	XX	PF 21-FEB-2003; 2003WO-US005241.
PR	PR	22-FEB-2002; 2002US-0359461P.
PA	PA	(GENTECH INC.)
XX	XX	PDR, Clark H., Hunt B., Jackman JK, Schoenfeld JR;
PI	PI	Williams PM, Wood WI, Wu TD,
DR	DR	WP; 2003-721702/68.

N-PSDB; ADF76611.	141 GlySerPheArgGlyArgHisProLeuProGlySerAspSerGlnSerArgProArg 160
S X	481 AGGCGTACATTCGGGTGTCAGCTCCAGGAAACCCCTGAACTGAGCTGTCCTCTT 540
T T	161 ArgArgThrPheProGlyValAlaSerArgAspProGluArgAlaArgProLeu 180
T T	Claim 10: SEQ ID NO 286; 918pp; English.
S X	This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the invention.
Sequence 371 AA;	Length: 371
2	Matches: 364
	Conservative: 0
	Mismatches: 7
	Indels: 0
	Gaps: 0
Alignment Scores:	1.84E-194
Score: No.:	1.929, 0.0
Score: Score:	98.11%
Score: Local Similarity:	98.11%
Score: Identity Match:	98.32%
Score: 7	
21 ArgTrpValIleLeuSerMetGluThrSerSerAspAspSerCysAspSer 40	
121 TTGGCTTGATAATTGGAAACAGGACTCTAGAGTAAAGAAGAACTTAAAGAAATTTC 60	
1 MetAspIleArgValIleGlyIleProGlnIleAspLeuArgValIleLysAspIle 20	
61 AGATATGTAAGTGTGATTCATGCCAAACTCTGATCCCTGTGACAGTTGGACCC 120	
21 ArgTrpValIleLeuSerMetGluThrSerSerAspAspSerCysAspSer 40	
121 TTGGCTTGATAATTGGAAACAGGACTCTAGAGTAAAGAAGAACTTAAAGAAATTTC 60	
41 PheIleSerAspThrPheAlaAsnThrArgLeuGlnSerValIleGlyCysArgThr 60	
181 CGACGCCAGTGCAAGCCTCTGGACCTCTGGACTCTAGGAGTTTCAGGCCGGAGT 240	
61 ArgSerGlnCysArgHisSerGlyProLeuArgValAlaMetLysPheIleArgSer 80	
241 ACCAGGGGNCACACAAACAGGCTCCGGCACCCCTAGAGATTCTGTGACT 300	
81 ThrArgGlyAlaThrAspIleAspIleGluSerArgGlnProSerGluAsnSerValThr 100	
301 GATTCGAACCTGGATTCTAGAGAGTAAAGGGAAATTTGGAGAAAGGGCTTTA 360	
101 AspSerAsnSerAspSerGluAspGluSerGlyMetAspIleGluGlySerGluAlaLeu 120	
361 AATATAAAAGAAAACAAACCAATGTTGCAAATCTCATGCTGAATTAGAAAGCTTCCT 420	
121 AsnIleLysIleAsnLysAlaMetIleAlaLysLeuMetSerGluSerPhePro 140	
421 GGCTCGTTCTGGTGAAGAACATCCCTCCAGGCOCGACTCAATCTAGGAGACCC 480	
	OS Homo sapiens.
	XX
	DN WO2003042661-A2.
	PN
	XX
	PD 22-MAY-2003.
	XX
	PF 13-NOV-2002; 2002WO-US036810.
	XX
	13-NOV-2001; 2001W0-035066P.
	XX

PR	21-NOV-2001;	2001US-0332464P.	QY	161 CGGAGCCAGTGAGGCCACTCTGGACCTCTCAGGTGGGATGAAGTTTCCAGGGTGGGAGT 240				
PR	03-DEC-2001;	2001US-033539P.	Db	61 ArgSerGlnCysArgHisSerGlyProLeuArgValAlaMetLysPheProAlaArgSer 80				
PR	14-DEC-2001;	2001US-034376P.	QY	241 ACCAGGGAGGCCAACCAACAAAAGGCAGTCCGCCAGCCCTCAGGAATTCTGTGACT 300				
PR	08-JAN-2002;	2002US-034721P.	Db	81 ThrArgGlyAlaThrAsnLysAlaGluUserArgGlnProSerGluAsnSerValThr 100				
PR	10-JAN-2002;	2002US-034734P.	QY					
PR	08-FEB-002;	000US-035525P.	Db					
PR	20-FEB-2002;	2002US-035907P.	QY	301 GATTCCAACCTCCGATTCAGAAAGTGAAGTGGATGATTTTGGAGAAAAGGCTTTA 360				
PR	29-MAR-2002;	2002US-036800P.	Db	101 AspSerAsnSerAspSerGluAspGluUserGlyMetAsnPhelLeuGluUserPhePro 120				
PR	04-APR-2002;	2002US-037011P.	QY	361 ATATTAAGGAAACAAAGCAATGCTGCAAAACTCATGTCAGGAACTTCCTCCT 420				
PR	12-APR-2002;	2002US-037224P.	Db	121 AsnLysGluAsnLysAlaMetLeuAlaLysLeuMetSerGluLeuGluUserPhePro 140				
PR	05-JUN-2002;	2002US-038661P.	QY	421 GGCGTGTTCGTTGGAGACATCCCTCCAGGTGGACTCAAATCAGGAGACCGCGA 480				
PR	16-JUL-2002;	2002US-039775P.	Db					
PR	22-JUL-2002;	2002US-039783P.	QY					
PR	03-SEP-2002;	2002US-040945P.	Db					
XX	(BOSB-)	EOS BIOTECHNOLOGY INC.	QY					
PA			Db	141 GlySerPheArgGlyArgHiProLeuProGlySerAspSerGlnSerArgArgProArg 160				
XX	Afar D.	Aziz N.	Ginsburg WM,	Gish KC,	Glynn R,	Hevezzi PA;	QY	481 AGGGTACATTCCGGGTTGGTTGCTTCCAGGAAACCTGAAAGGAGCTCTCCCT 540
PI	Mack DH,	Murray R,	Watson SR,	Wilson KE,	Zlotnik A;	XX	Db	161 ArgArgThrPheProGlyvalAlaSerArgGlyAsnProGluArgGluAlaArgProLeu 180
DR	WPI;	2003-468649/44.	QY	541 ACCAGGTCAAGGTCGGATTCCTGGCTCCCTGACGTCTACCATGRRGAGAGCCAGT 600				
DR	N-PSDB;	ADN40064.	Db	181 ThriArgSerArgSerArgLeuGlySerLeuAspAlaLeuProGluArgSerValAsnGlu 200				
XX	Determining the presence or absence of a pathological cell in a patient, comprising detecting a nucleic acid in a biological sample.	QY	601 TTGCAKRTMWTGTCATGTTGGTGTAGAGAGGAAACCGTGTACATGAAATCAA 660					
PR	useful for diagnosing, prognosing or treating cancer, comprising detecting a nucleic acid in a biological sample.	Db	201 GluGluAspLysTyrMetLeuValArglysArgSerThrValAspGlyTyrMetAsnGlu 220					
XX	SEQ ID NO 126; 1385pp; English.	QY	661 GATACCCCTCCCAAGGGTGGGATCATCGTGGACCCCTCCGATATAATTCCG 720					
CC	The invention relates to nucleic acids and proteins (ADN38683 - ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention, use of such antibodies for drug targeting; methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularis, strabismus syndromes, scarring and uterine fibroids. They may also be useful in wound healing, and in contraception. The present sequence represents a polypeptide of the invention.	Db	221 AspAspLeuProArgSerArgSerArgSerValProHisLeuProHisLeuPro 240					
CC	XX	QY	721 CCAGTGGAGAAATTACAGGAGGAGTTGGAGAACCTGCTGACAAATTCTGGAGAG 780					
CC	CC	Db	241 ProAlaGluLysLysLeuLysLysLeuLysLeuProHisLeuProHisLeuPro 260					
CC	CC	QY	781 ATATATAACCGTTCACTGGCTCTACTGCTCATGAACTATTGATGATACC 840					
CC	CC	Db	261 IleItyArgAsnArgSerLeuLysLysSerThrCysHisLysLysAspTrp 280					
CC	CC	QY	841 AAAACAAATGCAAAACCCAGATGCTGGGGCTTCAAGGCCGTTCTGGCCCTGC 906					
CC	CC	Db	281 LysThrAsnCysArgAsnProAspCysTrpGlyvalArgGlyLysProCys 300					
CC	CC	QY	901 CTTGAAACCGTTATGGTGTAGAGGCTACGGATCTGCTGGATCCGAACCTGCC 960					
CC	CC	Db	301 LeuArgAspArgTrpGlyLysGluValAlaGlyAlaLeuAspProAsnTriPhiScys 320					
CC	CC	QY	961 CCGCTTCTGCGAGGAATCTGCAACTCTGCAACTGCAACTGCTGGCAGCCAGTGGCTGG 1020					
CC	CC	Db	321 ProTrpCysArgGlyIleCysABCysSerProCysArgGlnArgAspGlyLysCysAla 340					
CC	CC	QY	1021 ACTGGGTCTTGTGTATTAGCAAAATCATGCTTGGCTGATGCTCTACTG 1080					
DB:	DB:	Db	341 ThriGlyValLeuValTyrIleAlaLysLysSerGlyLeuGlyAlaValAspIleLeu 360					
US-10-046-935-2234 (1-1116) × ADN38808 (1-371)	SQ	QY	1081 AAAACCTGAAACCGAATTGGATGCAAGCA 1113					
QY	1 ATGGACGCTGCCGCGCAGAAAAGATCTCAGAGTTAAAGAGAACTTAAAGAAATTC	Db	361 LysSerLeuLysGlnGluPheGluMetGlnAla 371					
DB:	1 MetAspAlaArgArgValProGlnLysAspLeuArgValAlaLysLysPhe 20	RESULT 6						
QY	61 AGATATGAGGTGTTATTCCATGAAACCTCGCATCCCTCTGATGACAGTTGNGACAGC	ADQ09178						
DB:	21 ArgTyrvAllylSleUleSerMetGluThrSerSerSerAspSerCysAspSer 40	ID	ADQ09178 standard; protein: 371 AA.					
QY	121 TTGGCTCTGATAATTGCAACACGAGCTGAGTCTGGGAAGGCTGAGGACC	XX						
DB:	41 PheAlaSerAspAsnPheAlaAsnThrArgLeuGinSerValArgGluGlyCysArgThr 60	AC	ADQ09178;					
DB:	23-SEP-2004 (first entry)	DT						

Human CDCA7/JP01 protein SEQ ID NO:363.
 X thanatos-associated protein; THAP; THAP responsive gene; THAP family;
 X THAP responsive element; angiogenesis; inflammation; metastasis; cancer;
 X apoptosis; cardiovascular disease; neurodegenerative disease; chemokine;
 X antiangiogenic; antiinflammatory; cardiovascular; cytoskeletal;
 X neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
 X human.
 X Homo sapiens.
 X WO2004055050-A2.
 X X 01-JUL-2004.
 D X 10-DBC-2003 ; 2003WO-IB006434 .
 F X 10-DEC-2002 ; 2002US-0432699P.
 R X 03-JUL-2003 ; 2003US-0485027P.
 R (ENDO-) ENDOCUBE SAS.
 K (CNRS) CNRS CENT NAT RECH SCI.
 A Girard J., Amalric F., Roussigne M., Clouaire T,
 A I
 K I
 K WPI ; 2004-525034/50.
 R N-PSDB; AUQ09179.
 R Modulating expression of a Thanatos (death)-Associated Protein (THAP)
 T responsive gene for preventing or treating, e.g., cancer or inflammation
 T comprises modulating the interaction of a THAP polypeptide with a nucleic
 T acid.

Example 45; SEQ ID NO 363; 612pp; English.

The present invention describes a method for modulating the expression of a THAP (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of the THAP responsive gene. Also described: (1) a method of modulating the expression of a gene responsive to a THAP/chemokine complex; (2) a pharmaceutical composition comprising a THAP responsive element in a pharmaceutical carrier; (3) a transcription factor decoy consisting essentially of a THAP responsive element; (4) a cell comprising a transcription factor decoy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP/chemokine complex; (6) a vector packaging cell line comprising a cell comprising a viral vector which comprises a promoter operably linked to a nucleic acid encoding a THAP family polypeptide or its biological fragment; (7) a method of constructing a cell which expresses a recombinant THAP-family polypeptide; (8) a method of ameliorating symptoms associated with a condition mediated by a THAP/chemokine complex; (9) methods of identifying a test compound that modulates transcription at a THAP responsive element or that modulates the transport of a chemokine into the nucleus; (10) methods for reducing the symptoms associated with a condition selected from excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease and neurodegenerative diseases; symptoms associated with a condition resulting from the activity of a chemokine or a THAP-family polypeptide in an individual; or symptoms associated with transcriptional repression or activation mediated by a THAP-family polypeptide in an individual; (11) a vector comprising a THAP responsive promoter operably linked to a nucleic acid encoding a detectable product; (12) a genetically engineered cell comprising the vector described above or that expresses a THAP-family polypeptide or its biological fragment; (13) an in vitro transcription reaction comprising a nucleic acid comprising a THAP responsive promoter, ribonucleotides and an RNA polymerase; and (14) an isolated murine THAP-family polypeptide that does not bind to a chemokine. The pharmaceutical composition has antiangiogenic, antiinflammatory, cardiovascular, cytotatic, neuroprotective and osteoprotective activities, and can be used as a THAP and THAP synthesis modulator. The composition can be used for

CC modulating the expression of a THAP responsive gene. Modulation is useful
CC for reducing symptoms of conditions such as excessive or insufficient
CC angiogenesis, inflammation, metastasis of a cancerous tissue, excessive
CC or insufficient apoptosis, cardiovascular disease or neurodegenerative
CC diseases. The present sequence is used in the exemplification of the
CC present invention.

Sequence 371 AA:						
Alignment Scores:	Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
Score: 1.84e-194	US-10-046-935-2234 (1-1116) x ADQ09178 (1-371)	1929.00	371	364	0	0
Percent Similarity: 98.11%	Qy	1	MetAspAlaArgValProGlnLysAspPleuArgValLysIleAsnLeuLys	60	0	0
Best Local Similarity: 98.11%	Db	1	MetAspAlaArgValProGlnLysAspPleuArgValLysIleAsnLeuLys	20	0	0
Query Match: 98.32%	Qy	61	AGATATCTGAATTGTATTCCATGGAAACCTCTCATCCTCTGATGACAGTTGTACAGC	120	0	0
DB: 8	Db	21	ArgTyrValLysLeuIleSerNetGlyThrSerSerSerAspPasserCysSsPsr	40	0	0
Qy	121	TTTGCCTCTGATAATTGCAACACAGGGCTGCACTCAGTTGGGAGGTCTTGAAGGCC	180	0	0	0
Db	41	pheAlaSerAspAsnHeAlaAsnThrArgLeuGlnSerValArgGluGlycSerArgThr	60	0	0	0
Qy	181	CGCACGGCACTGAGGCACTCTGACCTCTCAGGTTGGCATGAGTTTCAGGCCGGAGT	240	0	0	0
Db	61	ArgSerGlnCysSargHisSerGlyProLeuArgValAlaMetLysPheProAlaArgSer	80	0	0	0
Qy	241	ACCGGGGAGAACCAACACAAAAAGCAGAATGGGAAATGAACTCAGGCCCTOAGAGAA	300	0	0	0
Db	81	ThrArgGlyAlaThrAlnLysIleAlaGluSerArgGlnProSerGluAsnSerValThr	100	0	0	0
Qy	301	GATTCCAACCTCGATTCGAAGAATGAAACTCAGGTTGGAGAAAAGGCCCTTA	360	0	0	0
Db	101	AspSerAsnSerAspSerGluAspGluSerGlyMetAsnPheLeuGluLysAsnGalaLeu	120	0	0	0
Qy	361	AATATAAAGCAAACAAAGCAATGCTTGCAAAACTCATGTCGAAATTGAAAGCTCCCT	420	0	0	0
Db	121	AsnIleLysGlnAsnAsnlysAlaMetLeuAlaLysLeuMetSerGluLysGluSerPhePro	140	0	0	0
Qy	421	GGCTCGTCCGTGGAAAGACATCCCTCCCAGGGTCGACTCACATCAAGGAGCGCGA	480	0	0	0
Db	141	GlySerPheArgGlyArgHisProLeuProGlySerAspSerGlnSerArgGlyProArg	160	0	0	0
Qy	481	AGGGTACATTCGGGTGTTCCAGGAGAAACCCCTGAACGGAGAGCTCGTCCTCTNT	540	0	0	0
Db	161	ArgArgThrPheProGlyValAlaSerArgGlyAsnProGluArgGlyGlnSerVal	180	0	0	0
Qy	541	ACCAGGTCAAGTCCCCGATCTGGCTCCCTGAACTCTACCCATGRRGAGCCAGT	600	0	0	0
Db	181	ThrArgSerArgSerArgIleLeuGlySerLeuAspAlaLeuProMetGluGluGluGlu	200	0	0	0
Qy	601	TTKGAKRTMWTGATCATGTTGGATGGTCACTGAAAGGAGAAACCGTGGTACATGAA	660	0	0	0
Db	201	GluGluAspLysTyrMetLeuValArgLysGlyTyrMetAsdIu	220	0	0	0
Qy	661	GATGACTCTGCCAGAACGCCGTCAGATCATCCGTGACCCCTCGCATATAATTCGCG	720	0	0	0
Db	221	AspAspLeuProArgSerArgSerArgSerSerValThrLeuProHisLeuLys	260	0	0	0
Qy	721	CCAGTGAGAAGAAATTCAAGCAGGGCTGTTGAGAACCTCTGAGCAATTCTGAGAAG	780	0	0	0
Db	241	ProValGluGluIleThrGluGluGluSerAsnSerArgGlyLys	260	0	0	0
Qy	781	ATATAAACCGTTCACTGGCTCTACTTGTCAATGCGCTCAGAGACTATTGATACC	840	0	0	0

polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC79457 and AAC44240 represent sequences used in the exemplification of the present invention.

Alignment Scores:	
lignment Scores:	
ed. No. :	1.92e-194
core:	1929 00
arcent Similarity:	98.11%
est Local Similarity:	98.11%
erry Match:	98.32%
3:	3
3-10-046-935-2234 (1-1116) x AAB43720 (1-407)	
Y	1 ATGGACGTGCGCGATGGCGAGATCTCAGTAAAGAAGAACCTAAAGAAATTTC 60
Y	37 MetAspAlaArgAlaGlyProGlnLysAspLeuArgGlyValLysSerLysPhe 56
Y	61 AGATATGGAGGTGTTCCATGGAAACCTCGTGTATGCCATCTGTGACAGTGTCAGCAGC 120
o	57 ArgTrpValLysLeuIleSerMetGluThrSerSerSerAspSerAspSerAspSer 76
Y	121 TTTGCTTCGATAATTGAAAACCGAGGTGCACTGTTGGAAAGGCTGTGAGAAC 180
Y	77 PheAlaSerAspAspSerAlaAsnThrArgLeuGlnSerValArgGluGlySerGly 96
Y	181 CGCACCCAGTGCGACACTGGACCTCTCAGGGTGGCATGAACTTCCAGGGCGAGT 240
o	97 ArgSerGlnCysArgHisSerGlyProLeuArgValAlaMetLysPheProAlaArgSer 116
Y	241 ACCAGGGGACCAACCACAAACAAAAAGCAGAGTCGCCGCAGCCCTCAAGGAATTCTGTGACT 300
o	117 ThrArgGlyAlaThrAsnDybSlysAlaGluUserArgGlnProSerGluAsnSerValThr 136
Y	301 GATTCAAACCTCCGATTCAGAAGATCAGAAGTGAATGAAATTCTGGAAAGGGCTTTA 360
b	137 AspSerAsnSerAspSerGluAspGlyUserGlyMetAsnPheLeuGlyLysGly 156
Y	361 AATATAAGGAAAAACAAAGC2ATGCTTGCACAAACTCATGTCGATTAATTGAAAGCTTCCT 420
b	157 AsnLysGlnAsnLysAlaMetLeuAlaLysLeuMetSerGluIleGluSerPhePro 176
Y	421 GGCTGTTCGTTGGAGACATCCCCTCCAGGCTCGACTACAATAAGGAGACCGCGA 480
b	177 GlySerPheArgGlyArgHisProLeuProLysValAspSerGlnSerArgGlyArg 196
Y	481 AGGCCTACATTCCCGTGTGCTCCCTTGAGGCTCTAACCATGGRRGAGGCCAGT 540
b	197 ArgGlyThrPheProLysValAspArgGlySerGlyLysGlyArgPheLeu 216
Y	541 ACCAGGTCAAGGTCCGGATCCTCGGTCCCTTGAGGCTCTAACCATGGRRGAGGCCAGT 600
b	217 ThrArgSerArgSerArgIleLeuGlySerLeuAspAlaLeuProMetGluGluGlu 236
Y	601 TTGKGARKMTINWGTACATGTTGGTGAAGAGGGAAACCCGGTGTGATGGCTCATGATGAA 660
b	237 GluGluAspLysTyrMetLeuValArgLysArgLysGlyArgLysGlyArgPheLeu 256
Y	661 GATGAGCTGCCAGAAGGCGTGTGCTTCAAGATATCCGCTGACCTTCGGCATATAATTCG 720
b	257 AspAspLeuProArgSerArgSerArgSerArgSerValThrProHisIleLeu 276

Qy	721	CCAGTGGAAATTACAGAAGGAGTTATGGAGAACGCTCGGAACTTCGAGAGAG 780		that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
Db	277	ProValGluGluIleThrGluGluLeuGluAsnValcySerAsnSerArgGlyLys 296		XX
Qy	781	ATATAAACCGTTCACTGGCTCATCAATGCCGTCAGAGACTATTGTGACC 840		
Db	297	IleTyrAsnArgSerLeuGlyserThrCysGlnCysArgLysThrIleAspThr 316		
Qy	841	AAAACAACACTGCGAAACCCAGACTGTGGAGGTTGAGGCCAGTCTGTGCCCTGC 900		
Db	317	IystIleAsnCysArgAsnProAspCystrpGlyvalArgGlylnPheCysGlyProCys 336		
Qy	901	CTTCGAAACGGTTATGGTAGGAGCTGGATCGGAACTGGCATTG 960		Sequence 407 AA;
Db	337	IeuArgAsnArgTyrGlyIgluIvaArgAspAlaLeuLeuAspProAsnTrpHscys 356		
Qy	961	CGGCCPTGTCTCAGGAATCTGCAACTGCGAGTCTGCGGGCACGCGAGATGGCTGGCG 1020		
Db	357	ProProCysArgGlyIleCysAsnCysSerPheCysargGlnArgAspGlyIArgCysAla 376		
Qy	1021	ACTGGGCTCTCTGTATTAGCCAATAATCATGGCTTTGGAAATGTGCGAGCCCTACTTG 1080		
Db	377	ThrGlyValLeuValtryLeuIalystYtrIstIleGlyPheGlyAsnValHisAlaTyIleu 396		
Qy	1081	AAAAGCCTGAACAGAAATTGAAAGCAGA 1113		
Db	397	LysSerLeuIleysGlnGluPheGluMetGlnAla 407		
	RESULT	8		
ID	AAG74880	standard; protein; 407 AA.		
XX				
AC	AAG74880;			
DT	03-SEP-2001	(first entry)		
		Human colon cancer antigen protein SEQ ID NO: 5644.		
		Human: colon cancer: colon cancer antigen; diagnosis; detection; colorectal carcinoma.		
		Homo sapiens.		
		WO20012320-A2.		
		05-APR-2001.		
		28-SEP-2000; 20000W0-US026524.		
		29-SEP-1999; 99US-0157137P.		
		03-NOV-1999; 99US-0163280P.		
		(HUMA-) HUMAN GENOME SCI INC.		
		Ruben SM, Barash SC, Birse CE, Rosen CA;		
		WPI: 2001-235357/24.		
		N-PSDB: AAH34285.		
		Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.		
		Claim 11; Page 7194-7195; 9803pp; English.		
		AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytotoxic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome		
		AAH37195 and AAG73514 to AAG77788 represent human colon cancer antigens. The colon cancer antigens have cytotoxic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome		
		CCAGTGGAAATTACAGAAGGAGTTGGAGAACGCTCGGAACTTCGAGAGAG 780		
		GATGACTGCCAGAGCGTGGCTCATGCTGAGCATGCTACATGAAATGAA 660		
		TTKGARKMTMNGTACATGTTGCTGAGCATGCTACATGAAATGAA 720		
		AspAspIleuProArgSerArgSerArgSerArgSerValThrLeuProIleIleArg 276		

Db	261	fileTrAsnArgSerLeuGlySerThrCysIleSerGlnLysThrIleAspThr	280		Alignment Scores:	
Qy	841	AAAACAACCTGAGAACCAAGACTGTGGCGGAGATGGACGGTGTGGC	1020	Pred. No.:	6.42e-194	Length: 3.97
Db	281	LysThrAsnCysArgAsnProAspCysTrpGlyValArgIgYInPheCysGlyProCys	300	Score:	1924.00	Matches: 364
Qy	901	CTTCGAAACCTTATCTGTGAAGAGGTCAGGGATGCTCTGTGATCGAATTCG	960	Percent. Similarity:	97.85%	Conservative: 0
Db	301	LeuArgAsnArgTyrdLyGluValArgAspAlaLeuLeuAspProAsnTrpHisCys	320	Best Local Similarity:	97.85%	Indels: 7
Qy	961	CGCCCTTGTCAGGAGATCTGAACTCGAGTTCTGCCGAGATGGACGGTGTGGC	1020	Query Match:	98.06%	Gaps: 1
Db	321	ProProCysArgGlyIleCysAsnCysSerPheCysArgGlnArgAspGlyArgCysAla	340	DB:	6	
Qy	1021	ACTGGGGCTCTGTGTATTAGCCTAAATCATGGTGTGGAAATGTGCCTACTTGC	1080	US-10-046-935-2234 (1-1116) x ADA44119 (1-397)		
Db	341	ThrGlyValLeuValItyLeuAlaIstyHisGlyPheGlyAsnValIhsAlaIstyLeu	360	Qy	1 ATGGACGCTGGCGAGTTCATGAAACCTCGTCACTCCCTGTGACAGTGTGACAGTC	60
Qy	1081	AAAAGCCTGAAACAGGAAATTGAAATGCAAGGCAT 1114		Db	1 MetASPAlaArgArgValProGlnLysAspPheMetGluThrSerSerSerAspAspSerCysAspSer	20
Db	361	LysserLeu-AsnArgAsnLeuLysCysLysHis	371	Qy	61 AGATATGGAGGTAAATTCCATGAAACCTCGTCACTCCCTGTGACAGTGTGACAGTC	120
RESULT 10				Db	21 ArgTyrvAllysLeuIleSerMetGluThrSerSerSerAspAspSerCysAspSer	40
ADA44119				Qy	121 TTTGCTCTCTGATAATTGCAAACAGGAGCTGCAAGTC	180
ID	ADA44119	standard; protein; 397 AA.		Db	41 PheAspAspSerPheAlaAsnThrArgLeuInSerValArgGluGlyCysArgThr	60
XX				Qy	181 CGCACGCAGTCAGGCAACTCTGGACCTCTAGGTGGCATGAGTTCAAGCGGAGT	240
AC	ADA44119;			Db	61 ArgSerGlyDcysArgHissArgSerGlyProLeuArgValAlaMetLysPheProAlaArgSer	80
XX	20-NOV-2003	(first entry)		Qy	241 ACCGGGGGCCAACCAACAAAAGCAGAGTCCAGCCCTCAGGAGATTCTGTGACT	300
DT				Db	81 ThrArgGlyAlaIthrsNlysLysAlaGluSerArgGlnProSerGluAsnSerValThr	100
XX				Qy	301 GATTCGAACCTCGGATTCAAGAGTAAGTGGAAAGTGGCTTAACTGAAAGCTTCC	360
DE				Db	101 AspSerAspSerPheSerIluArgLysArgSerGlyMetAsnPhelLeuGlySerGluAsnSerVal	120
KW				Qy	361 AATAATAAGCAAAACAAANGCAATGCTGAATTCGAAAGCTTCC	420
KW				Db	121 AsnIleLysGlnAsnLysAlaMetLeuAlaLysLeuMetSerGluLeuSerPhePro	140
OS				Qy	421 GGCTCGTTCCGGTGGAAACGATCCCTCCAGGCTCGAGCTCTCCCT	480
XX				Db	141 GlySerPheArgGlyTyrGlyProLeuProGlySerAspSerGlnSerArgGlyProArg	160
OS				Qy	481 AGGGTACATTCGGGGTGTGGCTCAGGAGAAACCTGAACTGGAGAGCTC	540
XX				Db	161 ArgArgThrPheProGlyValAspSerGlyAsnProGluIaaArgProLeu	180
PN	WO200300865-A2.			Qy	541 ACCGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAG	600
XX	PD 03-JAN-2003.			Db	181 ThrArgSerArgSerArgIleLeuGlySerLeuAspAlaLeuProMetGluGluGluGlu	200
XX	PF 26-MAR-2002;	2002WO-US009105.		Qy	601 TPKGARKTMWGTACAGCTGTGAGAGAGAGAGAGAGCTCATGAAATGAA	660
XX	PR 27-MAR-2001;	2001US-0278650P.		Db	201 GluGluAspLysTyrMetLeuValArgLysSerGlyAsnGlySerValAsn	220
PR	12-SEP-2001;	2001US-00950082.		Qy	661 GATGACTCTGCCAGAACGCGTGGCTCCAGATCATCGTACCTTCGCAATAATGCG	720
PR	12-SEP-2001;	2001US-00950083.		Db	221 AspAspLeuProArgSerArgGlySerGlySerSerValLeuProHisIleArg	240
XX	PA (HUMA-)	HUMAN GENOME SCI INC.		Qy	721 CCAGTGGAGAATTACAGGAGGACTTGTGAGAGAGAGAGCTCTGAGAGAG	780
XX	PI	Rosen CA, Ruben SM;		Db	241 ProValGluIleThrGluGluLeuGluAsnValCysSerAsnSerArgGluLys	260
XX	DR	WPI; 2003-184045/18.		Qy	781 ATATATAACCGTTCACTGGGTCTACTGGCTACTTGTGATCATGCGTCAAGACTATTGCA	840
DR	N-PSDB;	ADA43929.		Db	261 IleTyRAsnArgSerLeuGlySerThrCysHisGlnLysThrIleAspThr	280
PT		A human secreted protein and nucleic acids useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating a diabetes or conditions related to diabetes, e.g. hyperglycemia, obesity, retinopathy, neuropathy, atherosclerosis, anaemia, stroke, gangrene, impotence, infection, cataract, renal disorders, or endocrine disorders. The present sequence was used to illustrate the invention.		Qy	841 AAAACAACCTGAGAACCCAGACTCTGGGGCTGAGCCAGTCAGGCACTTCTG	900
PT				Db	281 LysThrAsnCysArgAsnProAspCysTrpIlyvaArgGlyGlyInPheCysGlyProCys	300
PS	SEQ ID NO 311;	701pp; English.		Qy	901 CTTCGAAACCTTATGGTAGAAGAGCTAGGGATGCTCTGCTGGATCCGACTGGATTC	960
XX				Sequence 397 AA;		

Db 301 LeuArgAsnArgTyrglyGluGluValArgAspAlaLeuAspProAlaLeuAsp 320
 961 CGGCCCTTGATCGGAAATCGCACTGAGTTCTGGCCACCGGATGGACGGTTCGG 1020
 Qy 321 ProProTyArglyleCysSerCysSerPheCysArgGlnArgPheArgcysAla 340
 Db 1021 ACTGGGGCCCTGTGATTAGCCAAATAATCATGGGAAATGTCAGGCCTACTG 1080
 Qy 341 ThgIgyAlaLeuValtyLeuAlaValtyIleGlyArgIleGlyAsnValIleAlaTyrIeu 360
 Db ADC20449 standard; protein: 397 AA.
 Qy 1081 AAAAGCCCTGAACAGGATTGAAATGCCAAGCAT 1114
 Db 361 LysSerIeu-AasnArgAlaLeuIysCysIlysHis 371

RESULT 1.1
 ID ADC20449
 AC AC
 DT 18-DEC-2003 (first entry)
 XX Human secreted protein - amino acid sequence #130.
 DE gene therapy; human; secreted protein; haemopoietic disorder;
 KW haematological disorder; anaemia; haemophilia; inflammatory disorder; cancer;
 KW haematochemical bowel disease; Crohn's disease; neoplastic disease; cancer;
 KW leukaemia; wound healing; epithelial cell proliferation disorder;
 KW immune disorder; autoimmune disorder; asthmatic disorder;
 KW cardiovascular disorder; atherosclerosis; myocarditis;
 KW infectious disease; HIV; AIDS; endocrine disorder; diabetes;
 KW gastrointestinal disorder; duodenal ulcer; gastroenteritis;
 KW Homo sapiens.
 PN WO200292787-A2.
 PD 21-NOV-2002.
 PF 26-MAR-2002; 2002WO-US009257.
 PR 27-MAR-2001; 2001US-0278650P.
 PR 12-SEP-2001; 2001US-00950082.
 PR 12-SEP-2001; 2001US-00950083.
 XY (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 DR WPI; 2003-129287/12.
 XX New human secreted proteins and nucleic acid molecules, useful for diagnosing, preparing a diagnostic or pharmaceutical composition for diagnosing, preventing or treating hematopoietic or hematologic disorders, e.g. anemia or hemophilia.

PS Claim 1; SEQ ID NO 403; 1512pp; English.

XX The invention comprises the amino acid and coding sequences of human secreted proteins. The DNA and protein sequences of the invention are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating haematopoietic or haematological disorders (e.g. anaemia and haemophilia); inflammatory disorders (e.g. inflammatory bowel disease and Crohn's disease); neoplastic disease (e.g. cancer and leukaemia); wound healing and disorders of epithelial cell proliferation (e.g. immune disorders (e.g. autoimmune disorders and asthmatic disorders); cardiovascular disorders (e.g. atherosclerosis and myocarditis); infectious disease (e.g. HIV/AIDS); endocrine disorders (e.g. diabetes); and gastrointestinal disorders (e.g. duodenal ulcers and gastritis). The present amino acid sequence represents a human secreted protein of the invention.

XX Sequence 397 AA;

		Alignment Scores:	Length:
Pred. No.:	Pred.	6.42e-194	397
Score:		1924.00	Matches: 364
Percent Similarity:		97.8%	Conservative: 0
Best Local Similarity:		97.8%	Mismatches: 7
Query Match:		98.06%	Indels: 1
DB:		7	Gaps: 0
US-10-046-235-2234 (1-1116) x ADC20449 (1-397)			
Qy	1	ATCGACGCTCGGGCGAGAACATCGAGTAAGAGAATCTCGAGTAAGAGAACTTAAGGAAATTTC	60
Db	1	MetAspAlaArgArgValProGlnLysAspIleArgValLysAsnLeuIysLysPhe	20
Qy	61	AGATATGTAAGATTGATTGAAACCTCTCATCTCTGAAAGTGTGACAGTC	120
Db	21	ArgTyrValLysIleIleSerNetGluThrSerSerSerSerAspAspSerCysAspSer	40
Qy	121	TTCCTCTGATAAAATTGCAAACAGCAGGCTTCAGTCAGTTGGAGGGCTTAGGAC	180
Db	41	PheAlaSerAspAspPheAlaAsnThrArgLeuGluGluGlySerArgThr	60
Qy	181	CGCGGCCAGTCGCGGCACTCTGCAAGCTTCAGGGGGATGAAATTCAGGGCGGGACT	240
Db	61	ArgSerGlnCysArgHisSerGlyProLeuArgValAlaMetLysPheProAlaArgSer	80
Qy	241	ACCGGGGAGCACCAAAAGCAGTGTCCGCCAGCCCTAGAGAATTCTGTCAGT	300
Db	81	ThrArgGlyAlaThrAsnLysIleAlaGlyUserArgGinProSerGluAsnSerValThr	100
Qy	301	GATTCGAACATCCGATTCAAGATGAACTGGATGAAATTGAGAATTTTGAGAAAAGGCTTA	360
Db	101	AspSerAsnSerAspSerGluGlyNetAspPheLeuGluIleAspGluAlaLeu	120
Qy	361	AATATAAGCAAAAGCAATCTGAAACTCATGTCGATTAGAACTCTCCCT	420
Db	121	AsnLysGlnAnLysAlaMetLeuAlaMetLeuAlaLysLeuMetSerGluLeuUserIlePro	140
Qy	421	GGCTGTTCTGGAAAGCATCCCTCCAGGAACTGGTCCCGATCAGCATCAGGAGCCGCA	480
Db	141	GlySerPheArgGlyArgHisProLeuProGlySerAspSerGlnSerArgArgProArg	160
Qy	481	AGGGCTACATCCGGGTGTCTCCAGGAAACCCGAAACGGAGAGTCGTCCT	540
Db	161	ArgArgValIleSerArgSerArgLeuAspProLysGlyArgLysArgProLeu	180
Qy	541	ACCAGTCAGGTCGGGACCTCGGTCCCTGACGCTTACCCATGGAGAGCCAGT	600
Db	181	ThrArgSerArgSerArgIleLeuGlySerIleLeuLeuProMetGluGluGlu	200
Qy	601	TTKGARKMTWGTATGTTGATGTTGCTGAGAACCTGGTACATGATGAAATGAA	660
Db	201	GlutGluAspLysTyrMetLeuValArgLysArgLysThrValAspLysTyrMetAsnGlu	220
Qy	661	GATGACCTGCCAGAGCCGTCAGATCATCGTACCTGGCATATAATTGCG	720
Db	221	AspAspIleProArgSerArgSerArgSerSerValPhrIleProHisIleLeuArg	240
Qy	721	CCAGTGAAAGAAATTACAGGAGGGAGTTGAGAACGTCCTGAGGAACTTCGAGAGA	780
Db	241	ProValGluGluIleThrGluGluLeuAsnValCysSerAsnSerArgGluLys	260
Qy	781	ATATATACCGTTACGGGCTTACATCGTCATCATGCGATGAGACTATGATA	840
Db	261	IleTyrAsnArgSerSerIleGlySerIleGlySerIleGlySerIleGlySerIlePhe	280
Qy	841	AAACAACACTGAGAACCCAGACTGTCGGGAGCTGAGGAGCTGAGTCGCCCCTGC	900
Db	281	LysThrAsnCysArgAsnProAspCysIleGlyGlnPheCysGlyProCys	300
Qy	901	CITCGAAACCGTTATGGTAAAGGTAGGGATGCTGCTGATCGAACTGGCATTTGC	960

Db 301 LeuArgAsnArgTyrGlyGluValArgAspAlaLeuIeuAspProAsnTrpHisCys 320
 Qy 961 CCGCTTGAGGATCTGGAACTCGAGTTCTCGGGAGAGATGCCATTGTGGC 1020
 Db 321 ProProCysArgGlyIleCysAsnCysSerPheCysArgIlnAaspGlyArgCysAla 340
 Qy 1021 ACTGGGTCTTGTGCTTATTAATGCCAAATCATGGCTTGGAAATGTCATACTTG 1080
 Db 341 ThrGlyValLeuValtryLeuAlaLysTyrHisGlyPheCysIvaValIhsAlaTyrIeu 360
 Qy 1081 AAAAGCCCTGAACAGGAATTGTAAATGCAAGCAT 1114
 Db 361 LysSerLeu-LysAsnArgAsnLeuLysCysIysHis 371
 RESULT 12
 ADF10748 ID ADF10748 standard; protein; 397 AA.
 XX ADF10748;
 AC ADF10748;
 DT 12-FEB-2004 (first entry)
 XX Human secreted protein #70.
 DE HCDM64; HBHAA05; HBQCR46; HBKRD16; HCMSX51; HCOBH72; HDPPQ30; HE2CM39;
 KW HB9EA10; HGHPH91; HLDQ79; Cytostatic; Hepatotrophic; Antidiabetic;
 KW Antiinflammatory; neuroprotective; Anti-HIV; Vulnerary; Gynecological;
 KW Antineoplastic; Gene therapy; gastrointestinal disorder; cancer;
 KW Alzheimer's disease; chromosome identification.
 OS Homo sapiens.
 XX WO200299085-A2.
 PD 12-DEC-2002.
 XX PR 26-MAR-2002; 2002WO-US009135.
 XX PR 27-MAR-2001; 2001US-0278650P.
 PR 12-SEP-2001; 2001US-00950082.
 PR 12-SEP-2001; 2001US-00950083.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX WPI: 2003-221310/21.
 XX PT New human secreted polypeptides for diagnosing and treating neural,
 PT immune system, muscular, reproductive, gastrointestinal, cardiovascular,
 PT renal, and proliferative disorders and cancerous diseases.
 PS Claim 1; SEQ ID NO 211; 85ppr; English.
 XX The present invention relates to an isolated polypeptide chosen from 123
 CC human secreted proteins, such as, H6EDM64, HBHAA05, HBQCR46, HBKRD16,
 CC HBMSX51, HCQBR72, HDPQ30, HE2CM39, HE9EA10, HGBH91 and HLDQ79. The
 CC polypeptides are useful for the preparation of a diagnostic or
 CC pharmaceutical composition for diagnosing or and are useful for treating
 CC preventing diseases or conditions, such as neural, immune system,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative disorders and cancerous diseases and conditions. The
 CC polypeptides have immune activity, chemotactic activity, and binding
 CC activity to treat and prevent neuronal damage which occurs in certain
 CC neuronal disorders or neuro-degenerative conditions such as Alzheimer's
 CC disease, Parkinson's disease, and acquired immunodeficiency syndrome
 CC (AIDS)-related complex, and to prevent skin aging due to sunburn by
 CC stimulating keratinocyte growth. The molecules are also useful to
 CC modulate mammalian characteristics including, the encoding sequences are
 CC useful for chromosome identification, radiation hybrid mapping, in gene
 CC therapy, for identifying individuals from minute biological samples, as
 CC additional DNA markers for restriction fragment length polymorphism
 CC (RFLP), in forensic biology, molecular weight markers on Southern gels,

CC as diagnostic probes for the presence of a specific mRNA in a particular
 CC cell type, to raise anti-DNA antibodies using DNA immunization
 CC techniques, and as an antigen to elicit an immune response. The present
 CC sequence represents a human secreted protein of the invention.

RESULT 12;

DB: US-10-046-935-2234 (1-1116) x ADF10748 (1-397)

Qy	1 ATGGACGCTGCGCGATCTGAAAGATCTAGAGTAAGAGAAACTTAAGAACATTG 60
Db	1 MetAspAlaArgValProGlnLysAspLeuArgValLysAsnLeuLysIysPhe 20
Qy	61 AGATATGCAAGTGTGATTTCAGTGAACCTCTCATCCTCTATGAGACAGTTGTGACAGC 120
Db	21 ArgTyrrValLysBleuLysSerMetGluThrSerSerSerAspPheCysAspSer 40
Qy	121 TTGCTCTGTATAATTGCAAAACAGGCTGAGTAGTTCGGAGGGCTGTTAGGAC 180
Db	41 PheAlaSerAspAsnPheAlaSerThrArgLeuGlnSerValArgGluGlycysArgThr 60
Qy	181 CGCACGCAAGTGCAGGCCTCTGGACCCCTCAGGGTGCCTCAGGTTCCACGGCAGT 240
Db	61 ArgSerGlnCysArgHisSerGlyProLeuArgValAlaMetLysPheProAlaArgSer 80
Qy	241 ACCAGGGAGGCCACCACAAAGAGAGTCGCCAGCTTGGAAAGGGCTTTA 360
Db	81 ThrArgGlyAlaThrAsnLysSaiAlaGluUserArgSerGlnProSerGluAsnSerValThr 100
Qy	301 GATTCCAACTCCGATTCAGAAAGTGAATGAAATTGAAATTTGGAAAGAAAAGGGCTTA 360
Db	101 AspSerAsnSerAspSerGluAspGlyMetAsnPhoLeuGluLysArgAlaLeu 120
Qy	361 AATAAAAGAAAAACAGCAATGCTGCAAAGAAACTCTGTCTGAATAGAAGCTCTCC 420
Db	121 AsnIleLysGlnAsnLysAlaMetLeuAlaLysLeuMetSerGluLeuGluSerPhePro 140
Qy	421 CGCTCGTTCCGGTGGAAACACATCCCTCCAGCTCCACTACAATAAGGAGACCCGGA 480
Db	141 GlySerIleArgGlyIleHisIleLeuProGlySerAspSerGlnSerArgPheArg 160
Qy	481 AGGCPACATTCGGGGTGTCTCCAGGAAACCTCTGAACTCCATGRRGAGAGCCAGT 540
Db	161 ArgArgThrPheProDlyIyaAlaSerArgGargAsnProGluArgGaaArgPheLeu 180
Qy	541 ACCAGCTCAAGTCGGCTCCGGATCATGTCGCTTGTGAGCTCTACCCATGRRGAGAGCCAGT 600
Db	181 ThrArgSerArgSerArgIleLeuGlySerLeuAspAlaLeuProMetGluGluGlu 220
Qy	601 TTGKARKMTWGTACATGTCGGTGCAGAAGGAGCACTGGTGTGAGCTACATGAGTGA 660
Db	201 GluGluAspLysTyr-MetLeuValArgLysArgLysSerLeuAspGlyTyrMetAsnGlu 220
Qy	661 GATGACCTGCCAGAGCCCTGCTCAGATCATGGTACCCCTCCGCATATAATTGCG 720
Db	221 AspAspLeuProArgSerArgSerArgSerIleLeuProHisIleLeuIleArg 240
Qy	721 CCAGTCGAGAAATTACAGGAGGAGTGGAGAACGTCGTCAGCAAACTCTCGAGAGAG 780
Db	241 ProValGluIleThrGluGluLeuGluAsnValCysSerAsnArgClyLys 260
Qy	781 ATATATAACGGTCAACTGGCTCACTTGTCTCATCATGCGTCAGAAAGCTATTGATACC 840
Db	261 IleItyrAsnArgSerLeuGlySerThrCysHisGlnCysArgGlnLysIleAspThr 280

Qy 841 AAAACAACTCGAGAACCCGACTCTGGCGTGTGAGGCCAGTTCTGTCGCCCTGC 900
 Db 281 LysThrAsnCysArgAsnProAspCysTrpIleValArgGlyLysGlyProCys 300
 Qy 901 CTTCGAAAACCTTATGATGAGGGTCGGATGCTCTGCACTGGATTG 960
 Db 3001 LeuArgAsnArgArgArgIleGluLeuLysAlaLeuLeuAspProAsnTrpHisCys 320
 Qy 961 CGGCCCTTGTCGGAAATCTGCAACTGAGTTCTGCCGCAAGCAGATGGACCTGCG 1020
 Db 321 ProProCysArgGlyIleCysAsnCysSerProCysArgIleArgCysAla 340
 Qy 1021 ATCTGGGTCCTGTTGAAATTATCATGGCTTGCAATGTCATGCCCTACTG 1080
 Db 341 ThrGlyIleLeuValTyrLeuAlaLysTyrHisAlaTyrLeu 360
 Qy 1081 AAAAGGCTGAAACAGGAATTGAAATGCCAAGCAT 1114
 Db 361 LysSerIleu-AstArgAlaLeuIleCysIleIle 371

RESULT 13
 AB93122 standard; protein: 450 AA.
 ID AB93122
 XX AC
 XX AB93122;
 DT 26-JUN-2001 (first entry)
 XX Human protein sequence SEQ ID NO:12001.
 DE Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX Homo sapiens.
 XX EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PF 28-JUL-2000; 2000EP-00116126.
 XX 29-JUL-1999; 99-0B-00248036.
 PR 27-AUG-1999; 99-0B-00300253.
 PR 11-JAN-2000; 2000JB-00118776.
 PR 02-MAY-2000; 2000JB-0018367.
 PR 09-JUN-2000; 2000JB-00241899.
 XX (HELI-) HELIX RES INST.
 PA Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.;
 PI Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T.;
 DR WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX Claim 8; SEQ ID NO 12001; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in

CC gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH0316 to AAH13678 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB93893 represent human amino acid sequences; and AAH13632 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX Sequence 450 AA;

Qy Alignment scores:
 Pred. No.: 3.49e-189
 Score: 1879.50
 Percent Similarity: 60.89%
 Best Local Similarity: 80.89%
 Query Match: 95.80%
 DB: 4
 US-10-046-935-2234 (1-1116) x AAB93122 (1-450)

Qy 1 ATGGACGGCTCGCGCGTGCAGAAAGATCTCGAGCTAAAGGAACTTAAAGAAATT 60
 Db 1 MetAspAlaArgArgValProGlnIleAspLeuArgTallySlysLeuIysLysPhe 20
 Qy 61 AGATATGGAAGTTGATTGATTTCCATGGAACCTGTCTCATCCTCTGATGACAGTGTGACAGC 120
 Db 21 ArgTyrrValLysIleSerIleSerMetGluThrSerSerSerAspAspSerCysAspSer 40
 Qy 121 TTTGCTTCGATATAATTGCAAACACG 147
 Db 41 PheAlaSerAspAsnPheAlaAsnThrIysProLyssPheArgSerAspIleSerGluGlu 60
 Qy 147 ----- 147
 Db 61 LeuAlaSerValPhyTyrGluAspHisCysGlyPheSerCysGlyPheSerGluUser 80
 Qy 147 ----- 147
 Db 81 GluValGlnAspValLeuAspHisCysGlyPheIleGinLysProArgProAspValThr 100
 Qy 147 ----- 147
 Db 101 AsnGluLeuAlaGlyIlePheHisAlaAspSerAspAspGluUserAspSerPheCysGlyPheSer 120
 Qy 148 ----- 148
 Db 121 GluSerGluIleGlnAspGlyMetArgLeuGlnSerValArgGluGlyCysArgThrArg 140
 Qy 184 AGCGAGTGCAGGCACTCTGGACCTCTCAGGGCTGGATGAAAGTTCCAGGGCGGAGTAC 243
 Db 141 SerGlnCysArgHisSerGlyProIleuAspGlyMetAsnProAlaSerThr 160
 Qy 244 AGGGAGCACCAACAAMAGGAGTCCGGCAGCCCCTCAGGAATTCTGTGACTGTAT 303
 Db 161 ArgGlyAlaThrAsnLysAlaGluSeSerGlnProSerGluAsnSerValThrAsp 180
 Qy 304 TCCAACTCCGATTGAGAATGAAAGTGGATTTTGGACAACGGCTTAAAT 363
 Db 181 SerAlnSerAspSerGluAspGlyMetAsnProAlaSerThr 200
 Qy 364 ATAAGGCAAAACAAAGCCAATGCTGCAAACACTCATGTCGAAATTAGAAAAGCTTCCTGGC 423
 Db 201 IleLysGlnAsnLysAlaMetLeuIalysLeuMetSerGluLeuGluSerPhenProGly 220
 Qy 424 TCGTTCCTGGAAAGACATCCCTCCAGGETCCGGCTCAAAATCAAGGACACGGCAAGG 483
 Db 221 SerPheArgGlyIleGlyProLeuProGlySerIleSerArgGlyProIleArg 240
 Qy 484 CGRACATTCGGGTTGCTTCGGAGAACCTGAAAGGAGCTCGNCTCTTAC 543
 Db 241 ArgThrPheProGlyValAlaSerArgArgAsnProGluIargArgProLeuThr 260

Qy	544	AGGCTAAGGTCGGATCCTCGGTCCCTTGACGCTTACCCATGRRGAGGCCAGTTK	603
Db	261	ArgSerArgSerArgLeuAlaLeuProMetGluGluGluGlu	280
Qy	604	GASKMTMGTACATGTTGCTGAGAAAGAGAACCGTGGATCATGCGATTAATTGAAATGAGT	663
Db	281	GluAspLysTyrMetLeuValArgIysArgLysThrValAspAlaLeuProMetGluGluGluGlu	300
Qy	664	GACCTGCCAGAACGGTGCCTCCAGATCATCCNGACCCCTCCCATATAATTGCCCA	723
Db	301	AspLeuProArgSerArgSerArgSerArgSerValThrLeuProHsleLeuPheProIleLeuPhePro	320
Qy	724	GTGGAAGAAATTACAGGGAGACTGGAGAACCTCTGGAGCAATTCTGGAGACAGATA	783
Db	321	ValGluGluIleThrGluGluIleGluAsnValCysSerAsnSerArgGluLysIle	340
Qy	784	TATACCGTTCACTGGCTCTACTTGTCTAAATGCGTCAGAGACTATTGATACAAA	843
Db	341	TyrAsnArgSerLeuGlySerThrCysHisGlnCysArgGlnlysThrLeuAspThrIys	360
Qy	844	ACAAACTCGAGAACCCAGACTGTTGGCCAGTCTGGAGCCAGTCTGAGGCCCTTGCCTT	903
Db	361	ThrAsnCysArgAsnProAspCysTrpGlyValArgGlyInpheCysCysLysProCysLeu	380
Qy	904	CGAACACGGTTATGGTAAAGAGCTGAGGGATCTGGCTCGATCGAACCTGGCATTCGCCCTGGCCG	963
Db	381	ArgAsnArgGlyGluValArgAspAlaLeuLeuAspProAsnTrpHisCysPro	400
Qy	964	CCTTGTCAGGAATCTGAAACTCGATGTTCTGGGGCAATCTGCATGCCCTGGCGACT	1023
Db	401	ProCysArgGlyIleCysAsnCysSerProAspCysTrpGlyValArgGlyInpheCysCysLeu	380
Qy	1024	GGGGTCCCTTGTTGTTATTTAGCCAAATAATCATGGCTTTCGGCAATCTGCATGCCCTACTTGAA	1083
Db	421	GlyValLeuValTyRLeuAlaLysTrpIleGlyPheGlyAsnValHisAlaTyRLeuIys	440
Qy	1084	AGCCTGAAACAGGAAATTGAAATGCCAGCA	1113
Db	441	SerLeuIysGlnGluPheGluMetGluIala	450
RESULT 14			
DE	ADL91540	Human immune-related polypeptide PRO69531, SEQ ID NO:55.	
ID	ADL91540	standard; protein; 450 AA.	
XX			
AC	ADL91540;		
XX			
DT	17-JUN-2004	(first entry)	
XX			
DE			
XX			
KW			
KW		Human; PRO; activated T cell; immune-related; drug screening; detection;	
KW		stimulation; immune response; stimulation; diagnosis; immune disorder;	
KW		systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;	
KW		juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis;	
KW		idiopathic inflammatory myopathy; Sjogren's syndrome;	
KW		systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;	
KW		autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;	
KW		immune-mediated renal disease; demyelinating disease;	
KW		idiopathic demyelinating polyneuropathy; Guillain-Barre syndrome;	
KW		chronic inflammatory demyelinating polyneuropathy; hepatobiliary disease;	
KW		inflammatory bowel disease; primary biliary cirrhosis;	
KW		Whipple's disease; autoimmune skin disease; gluten-sensitive enteropathy;	
KW		bullosis skin disease; autoimmune disease; contact dermatitis; psoriasis;	
KW		allergic disease; asthma; allergic rhinitis; atopic dermatitis;	
KW		food hypersensitivity; urticaria; eosinophilic pneumonia;	
KW		idiopathic pulmonary fibrosis; hypersensitivity pneumonitis;	
KW		transplantation associated disease; graft rejection;	
KW		graft-versus-host disease; immunosuppressive dermatological;	
KW		hepatotropic; nephrotropic; antiadreatic; antiasthmatic; antipsoriatic;	
KW		antiallergic;	
KW		antihaemic; antiarteriosclerotic; antiarthritic;	

KW neuroprotective; respiratory; antiinflammatory; gene therapy.
 XX Homo sapiens.
 XX WO2004024072-A2.
 XX PD 25-MAR-2004.
 XX PP 10-SEP-2003; 2003WO-US028317.
 XX PR 11-SEP-2002; 2002US-0410340P.
 XX PA (GETH) GENENTECH INC.
 XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
 PI Williams PM, Wood WI, Wu TD;
 XX DR 2004-329384/30.
 XX N-PSDB; ADL91539.
 XX PT New PRO nucleic acid, useful for preparing a composition for d
 PT or treating an immune related disorder, e.g., systemic lupus
 PT erythematosus in a mammal.
 XX PS Claim 10; SEQ ID NO 55; 199pp; English.
 XX CC The invention relates to isolated human immune-related polypep
 CC (designated PRO) and nucleic acids (ADL91486 ADL91587). The PR
 CC polypeptides are overexpressed in CD4+ T cells activated by an
 CC -1 or anti-CD3 anti-CD28 antibodies compared with resting T C
 CC useful as diagnostic markers and therapeutic targets for immuno
 CC disorders. The invention also relates to sequences of at least 80
 CC to the PRO nucleic acid and polypeptide sequences of the invent
 CC recombinant vectors and host cells comprising a PRO nucleic ac
 CC method for the recombinant production of a PRO polypeptide; an
 CC against a PRO polypeptide; fusion proteins comprising a PRO po
 CC methods of screening for compounds which modulate PRO polypept
 CC activity or expression; a method for detecting a PRO polypepti
 CC method of detecting an immune response in a mammal; a method f
 CC simulating an immune response in a mammal; and methods for di
 CC and treating immune related disorders. PRO polypeptides and nu
 CC are useful in the diagnosis and treatment of immune-related dis
 CC such as systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathy,
 CC scleritis, idiopathic inflammatory myopathy, Sjogren's syndrome,
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimm
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated
 CC disease, a demyelinating disease of the central or peripheral
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barré
 CC chronic inflammatory demyelinating polyneuropathy, hepatobiliary
 CC infections or autoimmune chronic active hepatitis, primary bili
 CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, int
 CC bowel disease, gluten-sensitive enteropathy, Whipple's disease,
 CC autoimmune or immune-mediated skin disease, bullous skin disease,
 CC erythema multiforme, contact dermatitis, psoriasis, allergic d
 CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
 CC urticaria, immunologic disease of the lung, eosinophilic pneumonitis,
 CC idiopathic pulmonary fibrosis, hypersensitivity pneumonitis,
 CC transplantation associated disease, graft rejection or graft-vers
 CC disease. The present sequence represents a human immune-related
 CC polypeptide of the invention.

Alignment Scores:	
Pred. No.:	3.49e-189
Score:	18.79-50
Percent Similarity:	80.89%
Best Local Similarity:	80.89%
Query Match:	95.80%
DB:	8
Length:	450
Matches:	364
Conservative:	0
Mismatches:	7
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Gaps:	1

1 ATGGAACGGCTGGCGGTGCCAGAAAGATCTCAGAGTAAGAGAACTTAAAGAAATTTC 60
 Db 1 MetAspAlaArgArgvalProGlnIlysAspLeuArgValIlysAsnLeuIlysPhe 20
 Qy 61 AGATATGTGAGGTGATTTCATGGAAACCTCGTCATCCTCTGATGACAGTTGACAGC 120
 Db 21 ArgTyrValIlysLeuIlesSerMetGluThrSerSerSerAspSerCysAspSer 40
 Qy 121 TTGCTTCTCTATAATTGGAAAACAG----- 147
 Db 41 PheAlaSerAspAsnPheAlaAsnThrIlysProlysProArgSerAspIleSerGluGlu 60
 Qy 147 ----- 147
 Db 61 LeuAlaSerValPheTyrgluAspSerAspGlyPheSerGluSer 80
 Qy 147 ----- 147
 Db 81 GluValGlnAspValLeuAspHisCysGlyPheLeuGlnIlysProArgProAspValThr 100
 Qy 147 ----- 147
 Db 101 AsnGluLeuAlaGlyIlePheHisAlaAspSerAspAspGluSerPheCysGlyPheSer 120
 Qy 148 ----- 148
 Db 121 GluSerGluIleGinAspGlyMetArgLeuGinSerValArgGluGlyCysArgIleArg 140
 Qy 184 AGCCAGTGCAGGCACTCTGGACCTCTCAGGTGGCATGAAAGTTCCAGGGGAGTACC 243
 Db 141 SerGlnCysArgHissSerGlyProLeuArgValAlaMetIlysPheProAlaArgSerThr 160
 Qy 244 AGGGAGGAGCCACAAAAAAGAGAGAGATCCGCAGCCTCAGAGAAATTCTGACAGAT 303
 Db 161 ArgGlyAlaIthrAsnLysIleAlaGluSerArgGlnProSerIleAsnSerValThrAsp 180
 Qy 304 TCCAAACTCGATTAGAGATGAAAGTGGAAATGAATTTTGGAGAAAAGGGCTTAAT 363
 Db 181 SerAsnSerAspSerGluAspGlyIleSerIlyMetAsnPhelLeuIlysArgAlaLeuAsn 200
 Qy 364 ATAAAGCAAAACAAGCAAGCATGCTGCAAAACTATGHTGAAATTAGAAAGCTCCCTGC 423
 Db 201 IleLysginAsnAlaMetIleAlaIlysLeuMetSerGluIleGluSerPheProGly 220
 Qy 424 TCTTCCCTGGAGACATCCCTCCAGCTGGACTCACAACTCAAGGAGCCGAGG 483
 Db 221 SerPheArgGlyIarglsproleProGlySerAspSerGluSerArgProArg 240
 Qy 484 CGTACATCCCGGGTGTGCTTCAGGAGAAACCCGAAACGGAGGTCTGTCTCTTAC 543
 Db 241 ArgThrSerGlyValAlaSerArgAlaProGluIargProIleLeuIlysArg 260
 Qy 544 AGCTCAAGGTCCGGATCCTGGTCCCTGAGCTCTACCATGRRGAGGCCAGTTK 603
 Db 261 ArgSerArgSerArgIleLeuGlySerLeuAspAlaLeuProMetGluGluGluGlu 280
 Qy 604 GARKTMWGIATGTTGGAGAAAGGAGGACCTGGTACATGATGAGAT 663
 Db 281 GluAspLysItrMetLeuValArgIlysArgysthrValAspGlyItrMetAsnGluAsp 300
 Qy 664 GACTGCCCCAGAGCCGCGCTCCAGATCATCGTACCCGCAATAATTGCCCA 723
 Db 301 AspLeuProArgSerGlySerArgSerSerValThrLeuProIleIleArgPro 320
 Qy 724 GFGGAAGAAATTACAGGGAGGAGGTCGAGAACGTCGAGCAATTCTGGAGAGATA 783
 Db 321 ValGluGluIleThrGluGluIleGluSerValCysSerAsnSerArgGluIlysIle 340
 Qy 784 TATAACGGTTACTGGCTCACTTGTGCAATGCGTGCAGAAAGCTATTGATACCAA 843
 Db 341 TyrAsnArgSerIleGlySerThrCysArgGlnLysThrIleAspThrIlys 360

Qy 844 ACAAACTGCGAGAAACCAGAGCTGCTGGCGGTGAGGGCCAGTTCTGTCGCCCTGCCTT 903
 Db 361 ThrAsnCysArgAspProAspCysSrrGlyIargIlyGinPheCysGlyProCysLeu 380
 Qy 904 CGAACACGGTTATGCGAGAGGGTCAGGGATGCTCTGCTGATCGAACCTGGCATTCGCCG 963
 Db 381 ArgAsnArgTyrGlyIgluIvalArgAspAlaLeuAspProAsnTrpIscsPro 400
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 Db 401 ProCysArgGlyIleCysAsnCysSerPheCysBrginArgAspGlyIargCysValThr 420
 Qy 1024 GGGERCTGTGTTATTAGCCAAATACTGGCTTGGAAATGTCATGCTACTTGAAA 1083
 Db 421 GlyValLeuValTyrIleGluIalIysGlyPheGlyAsnValHisAlaTyrLeuIys 440
 Qy 1084 AGCCCTGAAACAGGAATTGAAATGCAAAAGCAAGCA 1113
 Db 441 SerLeuIysGlnGluIpheGluMetGlnAla 450

Search completed: October 12, 2004, 15:12:46
 Job time : 127 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 12, 2004, 15:18:46 ; Search time 100 Seconds

Title: US-10-046-935-2234

Perfect score: 1962

Sequence: 1 atggacgtcgccgtgcc.....aatttgcataatgcagaaggataa 1116

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1356558 seqs, 32282953 residues

Total number of hits satisfying chosen parameters: 2713116

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published_Applications_AA.QFTM=fastan_-SUFFIXX=rabd -MINMATCH=0.1
-LOOPC1=0 -LOOPC2=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human0.cddi -LIST=45 -DOCAIGN=200 -THR SCORE=200 -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-NCPU=6 -ICPU=3 -NO_MMAPP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBLOCKS=100
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Database : Published_Applications_AA.*

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- /cgn2_6/prodata/2/pubpa/US60_NEW_PUB.pep.*
- /cgn2_6/prodata/2/pubpa/US60_PUBCOMB.pep.*

Summaries

Result No. Score Match Length DB ID Description

RESULT 1

US-09-878-128-2235

Sequence 2235, Application US/09878178

Patent No. US2002017752A1

GENERAL INFORMATION:

Applicant: Jiang, Yugui

Applicant: Harlockier, Susan L.

Applicant: Secrist, Heather

Title of Invention: COMPOSITIONS AND METHODS FOR THE THERAPY

File Reference: 210121.527

Current Filing Date: 2001-06-08

Number of Seq ID Nos: 2237

Software: FastSEQ for Windows Version 4.0

Seq ID No: 2235

Length: 371

Type: PRT

Organism: Homo sapiens

Feature: variant

Name/Key: variant

Location: (1)...(371)

Other Information: Xaa = Any amino acid

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

JJS-09-878-178-2235	Alignment Scores:	3.06e-178	Length:	371	Db	301 LeuArgAsnArgTyrGlyGluGluValAlaLeuLeuAspProAsnTriPheCys 320
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Score:	100.00%	Conservative:	0	Db	321 ProDroGlySerGlyIleSarCysSerPheCysBArglDaaGaspGlyArgCysAla 340	
Percent Similarity:	100.00%	Mismatches:	0	Qy	1021 ACAGGGGNCCTCTGTTATTAGCCAAATAATCATGGCTTCGAAATGCAATGCCTACTTG 1080	
Best Local Similarity:	100.00%	Indels:	0	Db	341 ThrdlyValLeuValIrrlyLeuIalyStyThiBglYpheGlyAsnValHisAlaTrLeu 360	
Query Match:	9.9.03%	Gaps:	0			
DB:	9					
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Db	1 MetAspAlaArgValArgValProGlnlySlysAsnLeuIrrlySlysPhe 20					
		RESULT 2				
		; Sequence 2235, Application US/10046935				
		; Publication No. US20020156011A1				
		; GENERAL INFORMATION:				
		; APPLICANT: Jiang, Yugu				
		; Harlicker, Susan L.				
		; APPLICANT: Sechrist, Heather				
		; APPLICANT: Wang, Ajun				
		; APPLICANT: Stolk, John A.				
		; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY				
		; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER				
		; FILE REFERENCE: 210121.52701				
		; CURRENT APPLICATION NUMBER: US/10/046,935				
		; CURRENT FILING DATE: 2002-01-15				
		; NUMBER OF SEQ ID NOS: 2239				
		; SOFTWARE: FastSEQ for Windows Version 4.0				
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		; LENGTH: 371				
		; TYPE: PRT				
		; ORGANISM: Homo sapiens				
		; FEATURE:				
		; NAME/KEY: VARIANT				
		; LOCATION: 197, 201, 203, 204				
		; OTHER INFORMATION: Xaa = Any Amino Acid				
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		Best Local Similarity:	100.00%	Mismatches:	0	
		Query Match:	99.03%	Indels:	0	
		DB:	13	Gaps:	0	
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		Qy	481 AGGGGTACATTCGGGTTGTGTCACAGGAGACTCTGCTCTCTCT 540	Db	61 AGATATGTGAAGTTGATTCATGAAACCTCGTCTATCCTCTGATGACAGTTGAGACAGC 120	
		Db	161 ArgArgThrPheProGlyValAlaSerArgAsnProGluAlaArgProLeu 180	Db	61 ArgSerGlyAlaThrAsnLysAlaMetLeuAlaLysIleSerGluLeuSerPhePro 140	
		Qy	541 ACCAGGTCAAGGTCCGGATCTGGTACCTGAGCTCACATCAAGGAGCCGTA 480	Db	21 ArgTyrValIrrlySlysIleSerGluLeuSerMetGlutThrSerSerSerAspSerSer 40	
		Db	141 GlySerPheArgGlyArgHsProLeuProGlySerAspSerGlnSerArgAspProLrg 160	Db	121 TTGGCTCTCTGATATTGCAACACAAGGGCTGCTGAGTTCCAGGGGGAGCT 180	
		Qy	481 AGGGGTACATTCGGGTTGTGTCACAGGAGACTCTGCTCTCTCT 540	Db	61 ArgSerGlyAlaThrAsnLysAlaMetLeuAlaLysIleSerGluLeuSerPhePro 80	
		Db	201 ***Glu*****TyrMetLeuValArglyBarglySthValArglyIrrlyMetAsnGlu 220	Db	41 PheAlaSerAspAsnPheAlaAsnThrArgLysIleSerValArgLuglyCysArgThr 60	
		Qy	661 GATGACCTGGCCAGAGCCCTCGTCCAGATCCTGAGCTTACGGCTATATAATTGGC 720	Db	181 CGAGCCCCGCTGCAAGGACTCTGACACTCTGACACTCTGACACTCTGAC 240	
		Db	221 AspAspLeuProArgSerArgSerSerSerSerSerSerAspSerSer 200	Db	61 ArgSerGlyCysArgHsSerGlyProLeuArgAlaMetLysPheProAlaArgSer 80	
		Qy	721 CCAGCTGGAAATTACAGGAGGAGCTCTGCTGAGAACTTCTGAGAGAG 780	Db	241 ACCAGGGGAGCAACCAACAAANGCAGSTCCGCCACCCCTGAGAAATTCTCTGACT 300	
		Db	241 ProValGluLueIrrlySerIleGlySerIrrlySerIleAspPhe 280	Qy	841 AACAAACTGAGAACCCAGACTGCTGGGGCTGAGAACAGTCTGCCCCTGC 900	
		Qy	781 ATATATAACGGTCACTGGCTCTACTGCTCATCATGCTCAGAGACTTATGATA 840	Db	81 LysThrAsnCysArgAsnProAspCystGlyArgGlyGlnPheCysGlyProCys 300	
		Db	261 IleTyrAsnArgSerIleGlySerIrrlySerIleAspPhe 280	Qy	901 CATTGCAACTCCGATGCTGGAGGAGGTATGTGAGGAGGAACTTGGATCGAATGGC 960	

Db	261	IleTerAsnArgSerIleGlySerThrCysHisGlnCysArgGlnIleSerThrIleAspThr	280	Qy	121	TTCGCTTCTGATAATTGCAAAACAGGGCTGCAGTCAGTCAGTTGGGAAGGGCTGTAGAACCC 180
Qy	841	AAACACACTGAGAMACCAGACTGTGGGAGTTCAAGGCCAAGTCTGTCAGGCCCTGC 900	Db	41	PheAlaIleAspPheAlaAsnThrArgLeuGluSerValArgGluGlyCysArgThr 60	
Db	281	LysThrAsnCysArgAsnProaspCysTerpGlyvalArgGlyGlnPheCysGlyProCys 300	Qy	181	CGAGCCAGTGAGGCACTCTGACCTCTGACCTCTCAGGGTGGGATGAAAGTTCAGCGGGAGT 240	
Qy	901	CTTCGAAACCGTTATGGTAAGGGTCAAGGATGGCTCGATGGACTGGCATTCGATTCG 960	Db	61	ArgSerGlnCysArgHisSerGlyProLeuArgValAlaMetysPheProAlaArgSer 80	
Db	301	LeuArgAlanylArgTerGlyGluGluValArgAspAlaIleLeuIleAspTerThrIleCys 320	Qy	241	ACCGGGGAGGACACAACAAAGAGCAGTCAGGAAATTCTGACT 300	
Qy	961	CGCCCTTGTCGAGGAATCTGCAACTGCACTGAGTTCTGCCGCCAGGATGGACCGTGTGCG 1020	Db	81	ThrArgGlyAlaThrAsnLysAlaGluSerArgGlnProSerGluAsnSerValThr 100	
Db	321	ProProCysArgGlyIleCysBacNcySerPheCysArgGlnArgAspGlyArgCysAla 340	Qy	301	GATTCAACTCCGATTCAGAAGATGAAAGTGGAAATTGGACAGTCAGGCCCTCAGAACTCTGACT 360	
Qy	1021	ACTGGGGCCTCTGTTAGCCAAAATCAGCTGGGATCCTGGGATCATGCTACTTG 1080	Db	101	AspSerAsnSerAspSerGluAspGluSerGlyMetAsnPheLeuGluIleAspAlaIleu 120	
Db	341	ThrGlyValLeuValTerValTerAlaLysTerAlaLysTerAlaIleGlyPheGlyAsnValHisAlaTerLeu 360	Qy	361	ATAATAANGCAGAACAAAGCAATGCTGAAATTAGAAAGCTTCCCCT 420	
Db	1081	AAAGGCTGAAACAGGAATTGAAATGAGCA 371	Db	121	AsnLeuIleLysGlnAsnLysAlaMetLeuAlaLysLeuWetSerGluLeuTerPhePro 140	
Qy	361	LysSerIleLysGlnAla 371	Qy	421	GGCTGTTCCGGAGAGCATCCCTCCAGGCTCCAGCTCACATCAAGGAGACCGCGA 480	
Db	141	GlySerPheArgGlyArgHisProLeuProGlySerAspSerGlnSerArgAspSerGly 160	Qy	481	AGGGTACATTCCGGGTTGCTCCAGGAAACCTGAAACCTGAACTCCCTGCCTCTCT 540	
Db	161	ArgArgGlnPheProGlyValAlaSerArgArgAsnProGluArgAlaArgProLeu 180	Qy	541	ACCGGTCAAAGGTCGGGATCCMGGGTCCTTACCGCTACGGAGAGGCCAGT 600	
Db	181	ThrArgSerArgSerArgIleLeuPheAlaLeuPheAlaLeuPheAlaLeuPheAla 200	Qy	601	TTKAKRMTWFGTCATGTGGCAGAACAGGAGAACGTCATGAAATGAAATGAA 660	
Db	201	***Glu*****TerMerLeuValArgLysArgGlySerValAspGlyTerMeAsnGlu 220	Qy	661	GATGACCTGCCCCAGAACGCCCTCCGCAATCATCGAACCCCTCCGATATAATTTCGC 720	
Db	221	AspAspLeuProArgSerArgSerArgSerValSerTerLeuProHisIleLeuArg 240	Qy	721	CCAGCTGGRAGAAATTACAGGGGGAGTTGGAGAACCTGCTGAGAAATTCTGGAGAAG 780	
Db	261	IleTerAspArgSerIleGlySerThrCysHisGlnLysThrIleAspPheThr 280	Qy	721	FILETYPEASCP 720	
Db	281	ProValGluGluIleThrGluGluIleGluAsnValCysSerAsnSerArgGluIlys 260	Qy	841	AAAACAACCTGCAAAACCCAGACTCTGGGGCCTTCAGGCCAGTTCTGGCCCTCGC 900	
Db	301	LeuArgAsnArgTerGlyGluGluValArgGlyGlnPheCysGlyProCys 320	Qy	901	CCTCGAAACCCGTTATGGTGAAGAGGNCAGGGATCTGCTGGATGCACTGGAATTTGG 960	
Db	341	ThrGlyValLeuValTerValTerAlaLysTerAlaIleGlyPheGlyAsnValHisAlaTerLeu 360	Qy	961	CGCCCTTGTGAGGAACTGCAACTCTGCAAGGATCTGGCTGGGATGAGCTGGCTGCG 1020	
Qy	1	ATGGACGCTGCGCGTGCCTGCAAGATCTGAGCTTAAGAAATTTC 60	Db	321	ProProCysArgGlyIleCysAsnCysSerCysArgGlnArgAspGlyArgCysAla 340	
Db	1	MetAspAlaArgArgValProGlnLysAspIleSerMetGluThrSerSerSerAspSerCysAspSer 40	Qy	1021	ACTGGGGTCCCTGTTATTTAGCCAAATATCATGGCTTGTGCAATGCTACTTG 1080	
Db	21	ArgTerValLeuValTerValTerAlaLysTerAlaIleGlyPheGlyAsnValHisAlaTerLeu 360	Qy	1081	AAAAGCTGAAACGAAATTGAAATGCAACCA 1113	
Db	361	LysSerIleLysGlnGluPheGluMetGlnAla 371	Db	361	Sequence 16, Application US/10301822 Publication No. US20030148410A1 ; GENERAL INFORMATION:	

APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schiegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND COMPOSITIONS, KITS, AND THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-0292RNM
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-01-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 16
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-16

Alignment Scores:
Pred. No.: 6.87e-177 Length: 371
Score: 1929.00 Matches: 364
Percent Similarity: 98.11% Conservative: 0
Best Local Similarity: 98.11% MisMatches: 7
Query Match: 98.32% Index: 0
DB: 14 Gaps: 0

US-10-046-935-2234 (1-116) × US-10-301-822-16 (1-371)

QY 1 ATGGACGCTGCCGCGTCAAGCCAGAAAGATCTCAGATAAGAGAACTTAAGAAATT 60
Db 1 MetAspAlaArgArgValProGlnLysAspLeuArgValAsnLeuLysSlySph 20

QY 61 AGATATGTAAGTGTATTTCATCGAAAACCTCGTCACTCTGTAGTACAGTTGTGACGC 120
Db 21 ArgTyrValLysLeuIleSerMetGluThrSerSerAspSerSerAspSer 40

QY 121 TTGCTCTTGATAATTTCGAAAACAGGAGCTCAGTTGGGAAGGCTGTGACGC 180
Db 41 PhenylasSerAspAsnPheAlaAsnThrArgLysInserValArgGluLycsArgThr 60

QY 181 CGCACGCCAGTGCAGGCACTCTGACACTCTCAGGTGGCATGAGTTCCAGGGGAGT 240
Db 61 ArgSerGlnCysArgHisSerGlyProLeuArgValAlaMetLysPheProAlaArgSer 80

QY 241 ACAGGGAGCACCAAAAGAGCAGATGCTCCGCCTCAGAAATTCTGTGACT 300
Db 81 ThrArgGlyAlaThrAsnLysAlaLysUserArgGlnProSerGluAsnSerValThr 100

QY 361 AAATAAARGCAAAACAAGCAAGCTGCAAAACTCTGCAATTAGAAAGCTRCCT 420
Db 121 AsnLeuLysGlnAsnLysAlaMetLeuAlaMetSerGluLeuGluUserPhePro 140

QY 421 GGCTCGTTCGGTGAAGCATCCCTCCAGGTCCACTCACAAATCAGGAAGCCCGA 480
Db 141 GlySerPheArgGlyArgHisProLeuProGlySerAspSerGlnSerArgGlyProArg 160

QY 481 AGCGGTACATCCGGGTGTGCTTCCAGGAGAACCTGAACTGAGAGCTCGTCCTCTT 540
Db 161 ArgArgThrPheProGlyValAlaSerArgGlnAsnProGluArgGlnArgProLeu 180

QY 541 ACCAGGTCAAGGTCGGATCCTCGGGTCCCTGACGCTCTACCCATGGAGAGGCCAGT 600
Db 181 ThrArgSerArgSerArgLeuGlySerLeuAlaLeuProMetGluGluGlu 200

QY 601 TTGARKRMWGTAAATGTTGAGAAAGGAGAACCTGAGCTGATCATGATGAA 660
Db 201 GluGluAspLysTyrMetLeuValArgLysArgLysThrValAspGlyTyrMetAsnGlu 220

QY 661 GATGACTCTGCCAGAGCCCTGCTCAGATCATCGTACCTTCGACATATAATTTCGC 720
Db 221 AspAspLeuProArgSerGlySerArgSerGlySerValProHisLeuLeuArg 240

QY 721 CCAGRGGAAGAAATTACAGAGGAGAATTCAGAGGAGAATCTCGAGAACCTCGAGAAG 780
Db 241 ProValGluLysIleGluGluLysAlaGluAsnValCysserAsnSerArgGluLys 260

QY 781 ATATATAACCGTTCACTGGCTCPACTTGTCAATGCGCTCAGAGACTATTGATACC 840
Db 261 IleTerAsnArgSerLeuGlySerThrCysHisGlnCysArgGlnLysThrLeuAspThr 280

QY 841 AAAAGAAACTGAGAAACCGAGACTGCTGGCCGCTTGAGGAGCTGCTGCAACTGCA 900
Db 281 LysThrAsnCysSagAsnProAspCysStrGlyValArgGlyGlnPheCysGlyProCys 300

QY 901 CTTCGA AACCGTTATGTTGAGAGCTCAGGGATGCTGCTGCAACTGCA 960
Db 301 LeuIgargIgargTyrGlyGluValAlaGluAspProAsnTrpHisCys 320

QY 961 CCGCCTTGTCGAGGAATCTGCAACTGCAACTGCAACTGCAACTGCAACTGCA 1020
Db 321 ProProCysArgGlyIleCysAsnCysSerPheCysAsnGlnArgAspGlyArgCysAla 340

QY 1021 ACTGGGCTCTGTGATTAGCCTAAATCATGGCTTGGATATGCTACTCTG 1080
Db 341 ThrGlyValLeuValTyrIleAlaLysTerThrGlyPheGlyAsnValIleAlaTyrLeu 360

QY 1081 AAAAGCTGAAACAGGAATTGAAATGCAAGCAAGCA 1113
Db 361 LysSerLeuLysGlnGluGluMetGlnAla 371

RESULT 6
US-10-295-027-126
; Sequence 126, Application US/10295027
; Publication No. US20030223501
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and Tissues of Screening for Modulators of Cancer
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIORITY APPLICATION NUMBER: US 09/663,733
; PRIORITY FILING DATE: 2000-09-15
; PRIORITY APPLICATION NUMBER: US 60/350,666
; PRIORITY FILING DATE: 2001-11-13
; PRIORITY APPLICATION NUMBER: US 60/335,394
; PRIORITY FILING DATE: 2001-11-15
; PRIORITY APPLICATION NUMBER: US 60/332,464
; PRIORITY FILING DATE: 2001-11-21
; PRIORITY APPLICATION NUMBER: US 60/334,393
; PRIORITY APPLICATION NUMBER: US 60/340,376
; PRIORITY FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: US 60/347,211
 PRIORITY FILING DATE: 2002-01-08
 PRIORITY APPLICATION NUMBER: US 60/347,349
 PRIORITY FILING DATE: 2002-01-10
 PRIORITY APPLICATION NUMBER: US 60/355,250
 PRIORITY FILING DATE: 2002-02-08
 PRIORITY APPLICATION NUMBER: US 60/356,714
 PRIORITY FILING DATE: 2002-02-13
 Remaining Prior Application Data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOs: 1386
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 126
 LENGTH: 371
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-295-07-126

Alignment Scores:
 Pred. No.: 6.87e-177 Length: 371
 Score: 192.00 Matches: 364
 Percent Similarity: 98.11% Conservative: 0
 Best Local Similarity: 98.11% Mismatches: 7
 Query Match: 98.32% Indels: 0
 DB: 14 Gaps: 0

US-10-046-935-2234 (1-1116) x US-10-295-027-126 (1-371)

QY 1 ATGACCGTCGCCCCGTGCGCAGAAAGATCTAGAGTAAGAGAACCTTAAAGAAATTG 60
 DB 1 MetAspAlaArgArgValProGlnLysPheLeuLysSerGlyAlaAsnThrArgIle 20

QY 61 AGATATGAAAGTTGATTTCAATGAAACTCTGAGTGAAGTTGACGCC 120
 DB 21 ArgTyrvAllysLeuLysSerMetCluThrSerSerSerAspSerCysAspSer 40

QY 121 TTTGGTTCTGATAATTTCGAAACACGAGGCTGCAGTCAGTCCGGAAAGGCTGTAGGACCC 180
 DB 41 PheAlaSerAspAsnPheAlaAsnThrArgIleAsnThrArgIle 60

QY 181 CGCGCCASTGCGGCACTGGACACTGGCTCAGGTTGGCATGAAAGTTCCAGTTGCGGACT 240
 DB 61 ArgSerGlnCysArgBisSerGlyProLeuArgValAlaMetLysPheProAlaArgSer 80

QY 241 ACCAGGGAGAACCAAAGAACGAGTCCCACGCCCTGAGAAATTCTGTGACT 300
 DB 81 ThrArgGlyAlaThrAsnLysSerAlaGluUserArgGlnProSerGlnAsnSerValThr 100

QY 301 GATTCCAACTCGGATTCAGAGATGAAAGTGAATTTGGAGAAAAGGGCTTA 360
 DB 101 AspSerAsnSerAspSerGluAspGluUserGlyMetAsnPheLeuGluLysArgAlaLeu 120

QY 361 AATATAAAGCAAAACAAGCAATGCTGAAAGCTCATGCTGAAAGCTTCCCT 420
 DB 121 AsnIleLygInasnLysBALaMetLeuAlaLysLeuMetSerGluLeuSerPhePro 140

QY 421 GGCTCTTCCCTGGAGACATCCCTCCAGGCTCGACTCACAACTAGGAGACCGCGA 480
 DB 141 GlySerPheArgGlyArgHsProLeuProGlySerAspSerGlnSerArgProArg 160

QY 481 AGGGTACATCCGGGATGCTGAGGAGAACCTGAGCGAGAGCTGCTCTCT 540
 DB 161 ArgArgThrPheProGlyValAlaSerArgAsnProGluArgAlaArgProLeu 180

QY 541 ACCAGCTCAAGTCCCGATCCTCGGCTCCCTGAGCTTACCCGAGTGGAGAGCCAGT 600
 DB 181 ThrArgSerArgIleLeuGlySerLeuAspAlaLeuProMetGluGluGlu 200

QY 601 TTKGKARMTMNGTACATGTTGCTGAGAAGAGGAAGCCCTGATCATGATGAA 660
 DB 201 GluGluAspLysTyrMetLeuValArgLysThrAlaSpGlyTyrMetAsnGlu 220

QY 661 GATGACTGCGCAGAAACGCTCGCTCCAGATCATCGTGACCCCTCGCATATAATTGCG 720

Db 221 AspAspLeuProArgSerArgSerArgSerArgSerValThrLeuProHistLeuLeuArg 240
 Qy 721 CCAGTGGAAAGAAATTACAGAGGAGATGTTGAGAACCTCTGAGCACATTCTGAGAGAG 780
 Db 241 ProValGluIleThrGluIleGluGluAsnValCysSerAsnSerArgGluLys 260
 Qy 781 ATATATAACCGTTCACRGGCTCTACTGTGTCATCAATGCCCTGAGAAGACTATGATACC 840
 Db 261 IleTyrAsnArgerLeuGlySerThrCysHsSgIncySArgGlnLysThrIleAspThr 280
 Qy 841 AACACAAACTGAGAAACCAGACTGCTGGGGCGTTGAGGGCAAGTCTGCTGATCCCAACTGCAATGC 960
 Db 281 LysThrAsnCysArgAsnProAspCysTrpGlyValArgGlyGlnPheCysGlyProCys 320
 Qy 901 CTTGAAACCGTTATGGTGAAGAGTCAGGGATGCTGCTGATCCCAACTGCAATGC 1020
 Db 301 LeuArgAsnArgTrpGlyGluIvaValArgAspAlaLeuAspProAsnTrpHisCys 320
 Qy 961 CCGCCTTCGAGGAATCTGCAACTGCAAGTTCTGCGCGAGCAGGATGACCGTGTGCG 1020
 Db 321 ProTrcCysArgGlyIlecySarCysSerPheCysArgGlnArgAspGlyArgCysAla 340
 Qy 1021 ACTGGGCTCTCTGATTAGCCAAATATCATGGCTTGGGAATGTCATGCCTACTTG 1080
 Db 341 ThreIvaValLeuValtyIleuAlaLysTyrHisGlyPheGlyAsnValHisAlaTyrDeu 360
 Qy 1081 AAAGCCCTGAAAGGGATTGAAATGCAAGGAGCA 1113
 Db 361 LysSerLeuLysGlnGluPheGluMetGlnAla 371

RESULT 7
 US-10-046-935-2234
 ; Sequence 2-39, Application US/10046835
 ; Publication No. US20020156011A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Yugiu
 ; Harelocker, Susan L.
 ; APPLICANT: Sechrist, Heather
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Stolk, John A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
 ; FILE REFERENCE: 2101:21:52:1C1
 ; CURRENT APPLICATION NUMBER: US/10/046, 935
 ; CURRENT FILING DATE: 2002-01-15
 ; NUMBER OF SEQ ID NOS: 2239
 ; SOFTWARE: FastSEQ For Windows Version 4.0
 ; SEQ ID NO: 2239
 ; LENGTH: 391
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-046-935-2234
 Alignment Scores:
 Pred. No.: 7.02e-177 Length: 391
 Score: 1929.00 Matches: 364
 Percent Similarity: 98.11% Conservative: 0
 Best Local Similarity: 98.11% Mismatches: 7
 Query Match: 98.32% Indels: 0
 DB: 13 Gaps: 0
 US-10-046-935-2234 (1-1116) x US-10-046-935-2234 (1-391)
 Qy 1 ATGAGGCTCCCGCTGCCGAGAAAGATCTCAGGTAAGAAACTTAAAGAAATTTC 600
 Db 21 MetAspAlaArgArgValProGlnLysAspIleArgValLeuLysIleSphe 40
 Qy 61 AGATATGTAAGTGTGATTCCATGAAACCTGCTATCTCTGAGACAGTTGTGACAGC 1200
 Db 41 ArgArgValLeuLeuSerMetGluThrSerSerSerAspSerCysAspSer 60
 Qy 121 TTGCTCTGATAATTGCAAAACGCTCGCTCCAGATCATCGTGACCCCTCGCATATAATTGCG 180

Qy	721	CCAGCTGAAAGAATTACAGCAGGAGGTGGAAACGTTCTGCAGCAATTCTCGAGAGAAAG 780	Db	181 CGGAGCCAGTGGAGGCACTCTGAGACTCTGAGCTCTCAGGGGGATGAGTTTCAGGGGGACT 240
Db	261	ProValGluGluIleThrGluGluGluLeuAlaValCysSerAsnSerArgGlyLys 280	Qy	97 ArgSerGlnCysArgHisSerGlyProLeuAlaMetIysPheProAlaArgSer 116
Qy	781	ATATAAACCTTCACTGGGCTCTACTTGTGTCATCATGCCGTCAGAGACTTGTGATCC 840	Db	241 ACCAGGGGAGCACACCAAAAAGCAGAGTCCCAGCCAGAGATCTGAGAAATTCTGTGACT 300
Db	281	IleTyraSerArgSerIleGlySerThrCysHisGlnCysArgGlnIlySthrIleAspThr 300	Qy	117 ThrArgGlyAlaThrAlaIlySlysAlaGluSerArgGlnProSerGluAsnSerValThr 136
Qy	841	AAAACAACCTCGAGAACCCAGACTGTGGacGAGCAGTCTGTGGCCCCCTGC 900	Db	137 AspSerAsnSerAspSerGluaspGluSerGlyMetAsnPhelLeuGluIysAlaLeu 156
Db	301	LysThrAsnCysArgAsnProAspCystrpGlyValArgGlyIleCysGlyProCys 320	Qy	301 GATTCCAACACTCGGATTCAGAAGATGAAAGTGGAAATTGGAGAAAAGGCTTTA 360
Qy	901	CTTCGAAACCGTTATATGCTGAGGGTCAAGGTCTGCTGATCCGAAACTGGCATTCG 960	Db	117 ThrArgGlyAlaThrAlaIlySlysAlaMetLeuAlaIlySleuMetSerGluSerPhePro 176
Db	321	LeuGasnAArgTyrglyGluGluIvaArgAspAlaLeuLeuAspProAsnTrpHisCys 340	Qy	421 GGCTCGTTCCGTCGAAGAACATCCCTCCAGGGTCCGACTCAACATCAAGGAGC 480
Qy	961	CGGCTTGTTGAGGAATCTGCACTGAGTGTGTTGCGCGAGATGGGGTGGTGG 1020	Db	177 GlySerPheArgGlyArgIspLeuProGlySerAspSerGlnSerArgGlyProArg 196
Db	341	ProProCysArgGlyIleCysAsnCysSerPheCysArgGlnArgAspGlyArgCysAla 360	Qy	361 ATATAAACAAAGCAATGCTGCAAAACTCATGTCGCAATTAGAAAGCTTCCTCT 420
Qy	1021	ACTGGGCTCCGTGATTACCAAAATATCATGGCTTTCAGGAAATCTGCATGCCCTACTTG 1080	Db	157 AsnIleLysGlnIlySlysAlaMetLeuAlaIlySleuMetSerGluSerPhePro 176
Db	361	ThrGlyValLeuValIlyTyrrHsGlyIleGlySerCysArgSerIleGlySerLeu 380	Qy	481 AGGGTACATTCCGGGTTGTTGCTTCCAGGAGAAAACCTGAAAGGAGCTGCTCT 54
Qy	1081	AAAAGCTGAAACAGGAAATTGAAATGAAAGCA 1113	Db	197 ArgArgThrPheProGlyValAlaSerArgAsnProGluArgArgAlaArgProLeu 216
Db	381	LysSerIleLysGlnGluPheGluMetGlnAla 391	Qy	541 ACCGGTAAGGTCGCGATCTGGCTCCGCTTACCATGGAGAGCTGGCCAGT 600
Qy	601	TTKARKRQTMWGTACATGTTGGTACATGAAATGAAAGGAGAAACGGTGGATTAATGATA 660	Db	217 ThrArgSerArgSerArgGlyValAlaSerArgAsnProGluArgArgAlaArgProLeu 216
Db	237	GluIuaAspLysIstYmetIeuvaArgySargIystThrValApGlyTyrMetAsnGlu 250	Qy	661 GATGACCCTGCCAGAACGCGTCGCCAGATCATCGTGCACCTCTCCGCAATATAATTTCGC 72
Qy	661	ATATAAACCGTTCTACTTCTCATGAACTGGCTCTACTGCTTACGCTTACGCTTACGCTTAC 72	Db	257 AspAspLeuProArgSerZArgArgSerArgSerIleArg 270
Db	277	CCAGTGAGAAATTACAGGAGAGTGGAGACTGTCGACGCTGCAACATTCTGGAGAACG 78	Qy	721 CCAGTGAGAAATTACAGGAGAGTGGAGACTGTCGACGCTGCAACATTCTGGAGAACG 78
Qy	781	ATATAAACCGTTCTACTTCTCATGAACTGGCTCTACTGCTTACGCTTACGCTTACGCTTAC 84	Db	297 IleItyrasArgSerLendlySerThrCysHsiGlnCysArgGlnIlyThrIleAspThr 311
Db	841	AAAACAATGCAAAACCCAGACTGCGCCTTCAGGGCCAGTTCTGGCCACTGCAATTGTC 90	Qy	841 AAAACAATGCAAAACCCAGACTGCGCCTTCAGGGCCAGTTCTGGCCACTGCAATTGTC 90
Db	337	LysThrAsnCysArgAsnProAspCystrpGlyValArgGlyIinPheCysGlyProCys 35	Qy	901 CTTGAAACCGTATGGAGAGCTCAGGATGCTCTGCTGATCAGTGGCTATTGTC 96
Qy	961	CCGGCTTGTGAGGAACTCTGCAACTCTGGAGGATGCGAGTTCTCCGGAGGATGCGAGT 10	Db	337 LeuArgAsnArgTyrGlyIluIvalArgGlyAlaLeuLeuAspProAsnTrpHisCys 35
Db	357	ProProCysArgGlyIleSlysIstYmetIeuvaArgySargIystGlnIlyArgySala 37	Qy	1081 AAAAGCTGAAACAGGAAATTGAAATGCAATTGCAACTGCTCTGGAAATGTC 1113
Db	397	LysSerLeuIysGlnGluPheGluMetGlnAla 407	Qy	1021 ACTGGGCTCTGTGATTAGCCAAATATCATGCTCTGGAAATGTCGCTACTTG 10
Db	377	ThrGlyValLeuValIlyLeuAlaIlySlysAlaIlySlysAlaIlySlysAlaIlyLeu 391	Qy	377 ThrGlyValLeuValIlyLeuAlaIlySlysAlaIlySlysAlaIlySlysAlaIlyLeu 391
RESULT 9			Db	RESULT 10
US-09-925-301-1165			Qy	US-10-106-698-5654
; Sequence 1165, Application US/0925301			Db	; Sequence 5654, Application US/10106598
; Patent No. US200502308A1			Qy	; Publication No. US20050103690A1
; GENERAL INFORMATION:			Db	; GENERAL INFORMATION:
; APPLICANT: Rosen et al.			Qy	; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies			Db	; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and
; FILE REFERENCE: PA106			Qy	; CURRENT FILING DATE: 2001-05-10
; CURRENT APPLICATION NUMBER: US/09/925,301			Db	; PRIOR APPLICATION NUMBER: PCT/US00/05882
; CURRENT FILING DATE: 1999-03-12			Qy	; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 1694			Db	; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0			Qy	; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1165			Db	; SEQ ID NO: 1165
; LENGTH: 407			Qy	; LENGTH: 407
; TYPE: PRT			Db	; TYPE: PRT
; ORGANISM: Homo sapiens			Qy	; ORGANISM: Homo sapiens
US-09-925-301-1165			Db	US-09-925-301-1165
Alignment Scores:			Qy	US-10-046-935-2234 (1-1116) × US-09-925-301-1165 (1-407)
Pre. No.:	7.13e-177	Length: 407	Db	RESULT 10
Score:	1929.00	Matches: 364	Qy	US-10-106-698-5654
Percent Similarity:	98.11%	Conservative: 0	Db	; Sequence 5654, Application US/10106598
Best Local Similarity:	98.11%	Mismatches: 7	Qy	; Publication No. US20050103690A1
Query Match:	98.32%	Indeals: 0	Db	; GENERAL INFORMATION:
DB:	9	Gaps: 0	Qy	; APPLICANT: Ruben et al.
			Db	; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and
			Qy	; FILE REFERENCE: PA0001
			Db	; CURRENT APPLICATION NUMBER: US/10/106,698
Qy	1	ATGGACGCTCGCGCGTGCCTGAGGAAAGATCTGAGATAAGAGAACTTAAGAAATTTC 60	Qy	
Db	57	ArgTyraIlySleuIleSerMetGluThrSerSerSerAspSerCysAspSer 76	Db	
Qy	121	TTCGCTCTGTGATTAATTGCAAACCAAGCAGCTGGAACTGGCTTAGGAC 180	Qy	
Db	77	PheIleAspAsnPheIleAsnThrArgLeuIleSerValArgLeuIleSerValArg 96	Db	

QY 904 CGAAACCGTTATGGTCAAGGGTCGGATCTCTGGATCTCGAACCTGGCATTTGGCGAGATGGACGGTGGGACT 963
 DB 381 ArgasnArgyrglygluIvalArgAspAlaLeuIeuAspProAlnRphScysPp 400

QY 964 CCTGTGCGGAAATCTGAACTGCAGTTCTGCCGAGGAGATGGACGGTGGGACT 1023
 DB 401 ProcySarglyIleCysAsnCysSerPheCysArgIlnArgSpGlyArgCysAlaLthr 420

QY 1024 GGGGCTCTTGTTATTAGCCAATATCATGGCTTGGAAATGTGATGCTACTGGAA 1083
 DB 421 GlyValLeuValTyreIalaLysThrIleGlyPheCiyAsnValHisAlaTyrLeuLys 440

QY 1084 AGCTCTGAAACAGGAATTGAAATGCGAAGCA 1113
 DB 441 SerIleLeuGlyGluPheGluMetGlnAla 450

RESULT 12
 US-09-851-588-4
 Sequence 4, Application US/09851588
 Patent No. US2002042067AI
 GENERAL INFORMATION:
 APPLICANT: Mack, David
 APPLICANT: Gish, Kurt C.
 APPLICANT: Wilson, Keith B.
 TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITION
 OF SCREENING FOR COLORECTAL CANCER MODULATORS
 FILE REFERENCE: A-68829-1/DDB/JUD/AMS
 CURRENT APPLICATION NUMBER: US/09/851-588
 CURRENT FILING DATE: 2001-09-24
 PRIOR APPLICATION NUMBER: US 09 642, 252
 PRIOR FILING DATE: 2000-08-17
 PRIOR APPLICATION NUMBER: US 09/656, 002
 PRIOR FILING DATE: 2000-09-06
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 4
 LENGTH: 347
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-851-588-4

Alignment scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
1	1.48e-150	1656.00	97.41%	97.41%	9

Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
347	338	0	9	2	0

US-10-046-935-2234 (1-1116) x US-09-851-588-4 (1-347)

QY 1 ATGGACCGCTCGCCGTCGGATGGAACTCTGGATCTAGAGTAAGAACACTAAAGAACATT 60
 DB 1 MetAspAlaArgArgValProGlnLysAspLeuIleArgValLysLysAsnLeuLysPhe 20

QY 61 AGATATCTGAACTGGTGAATTCCATGGAAACCTCTGGATCTGAGACGTTGTGACAGC 120
 DB 21 ArgTyrValIleIleSerMetGluThrSerSerSerAspAspSerCysAspSer 40

QY 121 TTGGCTCTGATAATTCTCAAACACAGGCTGAGGCTGAGCTGGAAAGCTGGAGACC 180
 DB 41 PheAlaSerAspAsnPheAlaAsnThrArgLeuInSerArgLysGluGlyCysArgThr 60

QY 61 CGCAGCAGCTGGAGCACTCTGGACCTCTGGACCTCTGGTGGCATGAAGTTCCAGCGCGAGT 240
 DB 61 ArgSerGlnCysArgHissArgIlyProLeuArgValAlaMetLysPheProAlaArgSer 80

QY 241 ACCAGGGGAGCAACCAACAAAAGCAGACTCCCCCAGGCCCTAGAGAAATTCTGFGACT 300
 DB 81 ThrArgGlyAlaIthrAsnLysLysAlaGluUserArgInProSerIuABnSerVaThr 100

QY 301 GATGCCAACCTCCGATTAGAGATGAAATGGAATCAAATTGGAGAAAAGGGCTTAA 360

Db 101 AspSerAsnSerAspSerGluAspGluSerGlyMetAsnProLeuGluLysArgAlaLeu 120 ; PRIORITY APPLICATION NUMBER: US 60/350,666
 Qy 361 AATATAAGGAAACAAAGGAATGCTTGCAAAACCTATGCTGTGATTAGAACGCTCCCT 420 ; PRIORITY FILING DATE: 2001-11-13
 Db 121 AsnIleLysGlnAsnIleLysAlaMetLeuIleLeuMetSerGluLeuGluSerPhePro 140 ; PRIORITY APPLICATION NUMBER: US 60/335,394
 Qy 421 GGCTCGTTCCSTGGAGAACATCCCCTCCGGCTCGACTACAACTCAAGAGAACCGCGA 480 ; PRIORITY FILING DATE: 2001-11-15
 Db 141 GlySerPheArgGlyArgHsProLeuProLeuProLeuProLeuProLeuProLeu 160 ; PRIORITY APPLICATION NUMBER: US 60/332,464
 Qy 481 AGGCCTACATTCGGGGATGGCTTCAGGAGAAACCTGTAACGGAGCTCGTCCTCT 540 ; PRIORITY FILING DATE: 2001-11-21
 Db 161 ArgArgThrPheProGlyValAlaSerArgAsnProGluArgAlaArgProLeu 180 ; PRIORITY APPLICATION NUMBER: US 60/334,393
 Qy 541 ACCAGCTCAGGGTCCGGATCTCGGCTTCAGGCTCTACCGAGCTGGAGAGGCCAGT 600 ; PRIORITY FILING DATE: 2001-12-14
 Db 181 ThArgSerArgSerArgIleLeuGlySerLeuAspAlaLeuProMetGluGluGluGlu 200 ; PRIORITY APPLICATION NUMBER: US 60/347,211
 Qy 601 TTKGARKMTMWTGACATGTTGGTGTGAAAGAGGAGACCTGGTGTGATCATGATGAA 660 ; PRIORITY FILING DATE: 2002-01-08
 Db 201 GluGluAspIleValArgIleSArgySthrValAspGlyIleAsnGlu 220 ; PRIORITY APPLICATION NUMBER: US 60/356,714
 Qy 661 GATGACCTGGCCAGAGCCCTCGTCCAGTCATCGTGACCCCTCCGATATAATTGCG 720 ; PRIORITY FILING DATE: 2002-02-13
 Db 221 AspAspLeuProArgSerArgSerArgSerArgSerValThrLeuProHisIleLearg 240 ; Remaining Prior Application removed - See File Wrapper or PALM.
 Qy 721 CCAGNGGAAATTACAGA-GGAGCAGTTGGAGAACCTGGCAATTCTCGAG-AGA 778 ; NUMBER OF SEQ ID NOS: 1386
 Db 241 ProValGluIleIthrGluIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 260 ; SOFTWARE: PatentIn Ver. 2.1
 Qy 779 AGATATAAACCGTTACAGGGCTACTGTCTCATAAATGCCAGAAGACTATTGATA 838 ; SEQ ID NO: 1194
 Db 261 ArgYrIleThrValHistPraLeuValLeuAsnAlaValArgLeuLeuIle 280 ; LENGTH: 347
 Db 839 CCAAACAAACTGAGAACCCAACTGTTGGCCAGTTGTTGTTGCCCT 898 ; TYPE: PRT
 Db 281 ProlyGlnThrAlaGluThrGlnThrAlaGluAlaSerValAlaPro 300 ; ORGANISM: Homo sapiens
 Qy 899 GCCTTGAAACCAACGGTTATGGTGAAGGGTCAGGATGGCTGCTGGATCGGCTT 958 ; US-10-046-935-2234 (1-1116) × US-10-295-027-1194 (1-347)
 Db 301 AlaPheGluThrValMetVallyArgSerGlyMetLeuCystTrpIleArgThrGlyIle 320 ; Alignment Scores:
 Qy 959 GCGCGCCTTGAGGAATCTGCAAACTGCAATGTTCTGCGGCCAGGATGGACGGTGTG 1018 ; Pred. No.: 1 ATGGAGCTCGCCCGTGCAGCAGAACATCTCAGAGTAAGGAACTTAAAGAAATTIC 60
 Db 321 AlAArgLeuValGluGluSerAlaThrAlaValSerAlaGlySerGluMetAspGlyVal 340 ; Score: 1.48e-150 ; Length: 347
 Qy 1019 CGACTGGGTCCCTGTGTPAT 1039 ; Matches: 1656.0 ; Matches: 338
 Db 341 ArgLeuGlySerLeuCystIle 347 ; Percent Similarity: 97.1% ; Conservative: 0
 Db 361 AAATAAGAAAACAAAGCATGCTGCAAAACTCTGCTGAATTAGAAAGCTTCCT 120 ; Best Local Similarity: 97.41% ; Mismatches: 9
 Qy 121 TTGCTCTGTGATATTGCAACAGGAGCTCTGACCCCTCAGGGCGATGAGCTTGAGAC 180 ; Query Match: 84.40% ; Terminals: 2
 Db 41 PheAlaSerAspAsnPheAlaAsnThrArgLeuGlnSerValArgGlyGlyCysArgThr 60 ; DB: 14 ; Gaps: 0
 Qy 181 CGAGCAGTAGCGAGCAACTCTGAGGACTCTGACCCCTCAGGGCGATGAGCTTGAGAC 240 ; US-10-295-027-1194 (1-347)
 Db 61 ArgSerGlyCysArgHsSerGlyProLeuGlyProLeuGlyProLeuGlyProLeu 80 ;
 Qy 241 ACCAGGGAGCACCAACAAAGCAGTCCGGCCAGCTGAAATCTGCAACT 300 ;
 Db 81 ThrArgIYIAIthrAnlylysAlaGluUserArgGlnProSerGluAsnSerValThr 100 ;
 Qy 301 GATTCCAACTCGGATTAGAACATGAAGTGGATGATTTTGGAAAAGGGCTTA 360 ;
 Db 101 AspSerAsnSerAspSerGluAspGluSerGlyMetAsnProLeuArgGln 120 ;
 Qy 361 AAATAAGAAAACAAAGCATGCTGCAAAACTCTGCTGAATTAGAAAGCTTCCT 420 ;
 Db 121 AsnIleLeuGlyAsnIleAlaMetLeuIalysLeuMetSerGluLeuGluSerPhePro 140 ;
 Qy 421 GGCTCGTTCCGGTGAAGACATCCCTCCGACTCACAACTAGGAGACCGCGA 480 ;
 Db 141 GlySerPheArgGlyArgHisProLeuProGlySerAspSerGlnSerArgProArg 160 ;
 Qy 481 AGGCGR2ACATTCGGGTGTTGCTTCAGGAAACCTGACGGAGAGCTGTCCTCT 540 ;
 Db 161 ArgArgThrPheProGlyValAlaSerArgAsnProGluArgAsnProGluArgAlaArgProLeu 180 ;
 Qy 541 AATATAAGGAAATTACAGA-GGAGCAGTTGGAGAACCTGGCAATTCTCGAG-AGA 778 ;
 Db 201 ProValGluIleIthrGluIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 260 ;
 Qy 779 AGATATAAACCGTTACAGGGCTACTGTCTCATAAATGCCAGAAGACTATTGATA 838 ;
 Db 261 ArgYrIleThrValHistPraLeuValLeuAsnAlaValArgLeuLeuIle 280 ;
 Qy 839 CCAAACAAACTGAGAACCCAACTGTTGGCCAGTTGTTGCCCT 898 ;
 Db 281 ProlyGlnThrAlaGluThrGlnThrAlaGluAlaSerValAlaPro 300 ;
 Qy 899 GCCTTGAAACCAACGGTTATGGTGAAGGGTCAGGATGGCTGCTGGATCGGCTT 958 ;
 Db 301 AlaPheGluThrValMetVallyArgSerGlyMetLeuCystTrpIleArgThrGlyIle 320 ;
 Qy 959 GCGCGCCTTGAGGAATCTGCAAACTGCAATGTTCTGCGGCCAGGATGGACGGTGTG 1018 ;
 Db 321 AlAArgLeuValGluGluSerAlaThrAlaValSerAlaGlySerGluMetAspGlyVal 340 ;
 Qy 1019 CGACTGGGTCCCTGTGTPAT 1039 ;
 Db 341 ArgLeuGlySerLeuCystIle 347 ;
 RESULT 13 ;
 US-10-046-935-2234 ; Sequence 1194, Application US/10295-027
 ; Publication No. US200302350A1 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel ; APPLICANT: Murray, Richard
 ; APPLICANT: Aziz, Natasha ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Ginsberg, Wendy M. ; APPLICANT: LeinsterSerGluLeuGluSerPhePro
 ; APPLICANT: Gish, Kurt C. ; APPLICANT: Eos Biotechnology, Inc.
 ; APPLICANT: Glynn, Richard ;
 ; APPLICANT: Hevezsi, Peter A. ;
 ; APPLICANT: Mack, David H. ;
 ; APPLICANT: Murray, Richard ;
 ; APPLICANT: Watson, Susan R. ;
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 ; METHODS OF SCREENING FOR MODULATORS OF CANCER
 ; CURRENT APPLICATION NUMBER: US/10/295,027 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: US 09/663,733 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR FILING DATE: 2000-09-15

; TITLE OF INVENTION: Compositions, and Methods of Screening for Colorectal
 ; TITLE OF INVENTION: Cancer Modulators
 ; FILE REFERENCE: 018501_006141US
 ; CURRENT APPLICATION NUMBER: US-10/264,820
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: US 03/268,866
 ; PRIOR FILING DATE: 1999-03-15
 ; PRIOR APPLICATION NUMBER: US 09/435,945
 ; PRIOR FILING DATE: 1999-11-09
 ; PRIOR APPLICATION NUMBER: US 09/436,983
 ; PRIOR FILING DATE: 1999-11-09
 ; PRIOR APPLICATION NUMBER: US 09/450,857
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: US 09/453,850
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: US 09/493,444
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 09/525,993
 ; PRIOR FILING DATE: 2000-03-15
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 19
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human CGA7
 US-10-264-820-19

Alignment Scores:
 Pred. No.: 1.0e-136 Length: 320
 Score: 1512.50 Matches: 305
 Percent Similarity: 95.95% Conservative: 3
 Best Local Similarity: 95.02% Mismatches: 11
 Query Match: 77.09% Indels: 2
 DB: 14 Gaps: 1

US-10-046-935-2234 (1-1116) x US-10-264-820-19 (1-320)

Qy	82 ATGGAACCTCGTCATCCCTGTGACAGTCTGTGACAAGCTTTGCTCTGATAATTGGCA	141
Db	1 MetGluThrSerSerSerAspSerAspSerCysAspSerAspSerAsnHeAla	20
Qy	142 AACACGAGGCTGCACTGAGTCTGGAAAGGCTGTAGGACCCGCCAGCAGTGCCAGGACTCT	201
Db	21 AsnThrArgLeuGlnSerValArgGluGlyCysArgThrArgSerGlnCysArgIleSer	40
Qy	202 GGACCTCTAGGGTGGCATGACTTCAAGGGGAGTACGGGAGAACCAACAAA	261
Db	41 GlyProIleArgValAlaMetLysPheProAlaArgSerThrArgGlyAlaThrAsnLys	60
Qy	262 AAAGCCAGTCCGCAGGCCCTGAGAGATTCTGGACTCTGATTCACCTCGATTGAA	321
Db	61 LYSAlaGluSerArgSerGlnProSerGluSerSerAlaSerArgSerGluSerGlu	80
Qy	322 GATGAAAGTGGATGAAATTCTGGAGRAAGGGCTTAATAATAAGCAAACAAAGCA	381
Db	81 ASPGluUserGlyMetAsnPheLeuGlyLysArgAlaAsnLeuAsnLysAla	100
Qy	382 ATGCTTGCACAAACTCTGTCGAAATTGAGAACCTCCGCTCTGGCTGCTCGTGAAGCAT	441
Db	101 MetLeuAlaLysLeuMetSerGluLeuSerPheProGlySerPheArgGlyArgHis	120
Qy	442 CCCCTRCAGGCTCCGACTCAATCAGGAAACGCCAGGGTCAAGGCTACATCCGGGTGTT	501
Db	121 ProLeuProGlySerPheSerPheSerGlySerGlyProArgGlyArgThrPheProGlyVai	160
Qy	502 GCTTCAGGAGAAACCTGAACTGAAAGCTGCTGCTCTTACAGGTCAAGGCTCAAGGCTGCTG	561
Db	141 AlaSerArgAsnProGlyArgGlyArgSerArgSerArgSerArgSerArgLys	621
Qy	562 CTCGGCTCCCTTGACCTCTACCCAGGAGAACCTGAACTGAAAGCTGCTGCTG	621

BLANK

RESULT 2

QY 682 CGCTCCAGATCATCGTACCCCTCCGATATAATTGCCCACTGGAAATTACAGAG 741
 Db 201 ArgTrgArgSerValThrLeuProHisIleAspProValGluIle-Glnly 220
 QY 742 G---AGGACTTGAGAACCTCTGAGCAATTCTCGAGAGAAGATATAACCGTTCACTG 798
 Db 220 sGluArgSerTrpArgThrSerAlaAlaIleLeuGluLysIleIleThrAlaIstr 240
 QY 799 GGCTCTACTTGTATCATAANGCCCTCAGAAGAACTATTGATAACCCAAACAGAAC 858
 Db 240 pAlaIeuLeuValIleAsnAlaValArgLeuIleProlysGlnThrAlaGluH 260
 QY 859 CCAGACTGTGGCGCTTGAGGCCAGTTGCTGCCCTGCCTCTGAAACGGTTATG 918
 Db 260 rGlnThrAlaGlyAlaPheGluAlaSerSerValAlaProAlaPheGluThrValMetVa 280
 QY 919 GAAGGGTCAAGGATGCTCGCTGGATCGGAACCTGGCATTCGCCGCTTGTGAGGAATC 978
 Db 280 lLysArgSerGlyMetLeuCystPileArgThrGlyLeaLaaArgLeuValGluIle 300
 QY 979 TGCAGACTGCGATGTTCTGCCGGCAGGGTGGACTGGGTTCCCTGTGTGTAT 1038
 Db 300 rAlaThrAlaValSerAlaGlySerGluMetAspGlyValArgLeuGlySerIeuCysI 320
 QY 1039 T 1039
 Db 320 e 320

RESULT 3
 US-09-252-991A-20376
 ; Sequence 20376, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196_136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIORITY FILING DATE: 1999-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/074,788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/094,190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 20376
 ; LENGTH: 433
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20376

Alignment Scores:
 Pred. No.: 7.52e-05
 Score: 125.50
 Percent Similarity: 31.34%
 Best Local Similarity: 25.37%
 Query Match: 6.40%
 DB: 4

US-10-046-935-2234 (1-1116) × US-09-252-991A-20376 (1-433)

QY 343 TTGGAGAAAAGGGCTTTAAATAAAAGCAAACAAAGCAATGCTGAAACTCATGTCT 402
 Db 2 LeuIysAlaLeuAlaSerValMetArgAsnThrProGlySerLeuArgySthr-PheSer 21
 QY 403 GAATA-----GAAAGCTTCCCTGGCTGTTGCTGAAAGACATCCCCTCCCA 450
 Db 22 SerIeuProValProSerArgGlyPheProGlySerArgArgAaArg--ProPhePro 40

QY 451 GGTCGGACTCACAA-----TCAGG 471
 QY 41 AlasAspSerArgMetProSerGlyTrpProValProOysAlaGlyThrProArgArg 60
 QY 472 AGACCGCGAAGGGCTACATCCCGGGTGTGCTTCCAGGAACCCCTGAAACGAGAGCT 531

Db 61 SerThrArgArgSerAlaAlaGlySerAlaLeuArgArgThrProAlaGlySerVal 80
 QY 532 CGTCCTCT---ACCAGGTCAGGTCCCGATCCTCGGTCCCTGACCTCTACCATG 588
 Db 81 GlyProCysArgCysGluProArg-ProSerAlaAlaGlyProThrSer----ProTr 98
 QY 589 GRGAGGCCAGTTKGARKMTMGTACATGTTGTGAGAAAGGAAAGACCCGTTGATGCC 648
 Db 98 ppRALapro-----ArgAlaRpaLargArgAlaAla-----109
 QY 649 TACATGAAATGAAAGATGACTGCCAGAAGCCGTCAGATCATCGTGACCCCTCCG 708
 Db 109 -----109
 QY 709 CATAATAATTGCCAGTGGAAATAATCAGAGGAGGTGGAGAAACCTC-----759
 Db 110 -----123
 QY 760 -TGCAGCAATTCTGAGAAAGATAATAACCGITCACTGGGCTCTACTGTGTCATCAATG 818
 Do 123 yCysSerAlaAlaArgArg-----SerArgProThrArgCY 135
 QY 819 CGCTCAGAGACATTGATACCAAAACAAACTGCAGAACCCAGACTGTGGGGCGTRICG 878
 Db 135 saGserArgThrIleArgGlyIutnArglyAsnTrpSerProThrAlaGlySerAlaAar 155
 QY 879 A-----GGCCAGTTCTGTTGCCCTGCTTGCCTAACCGTTARGTGAAGGGTCAGGGA 932
 Db 155 gThrGlyProThrCysGlyProCys-----ArgTyr-----166
 QY 933 TGCTCTGGATCGAACTGGATTGCG-----166
 QY 933 TGCTCTGGATCGAACTGGATTGCG-----963
 Do 167 -----TrpArgTrpProPheArgProGlyThrProCys-----ArgTyr-----180
 QY 964 -----CCCTCTGAGGAAATCTGCAACTGC-----987
 Db 180 gSerProCysArgGlyProGlySerCysCysAsnArgAlaArgLeuProGlySerGlyArgYar 200
 QY 988 ---AGTTTCTGCCGGCAGCGA 1005
 Db 200 gGlySerAlaCysArgSerArg 207

RESULT 4
 US-09-976-594-375
 ; Sequence 375, Application US/09976594
 ; GENERAL INFORMATION:
 ; APPLICANT: Buchbinder, Jenny
 ; APPLICANT: Furness, Michael
 ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
 ; FILE REFERENCE: PA-0041 US
 ; PATENT NO. 6673549
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,409
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 1143
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 375
 ; LENGTH: 754
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. 6673549 3688791CD1
 ; US-09-976-594-375

DB:	4	Gaps:	12
US-10-046-935-2234	(1-1116)	x US-09-976-594-375	(1-754)
Qy	4 GACGCTGCCCGTGCAGAAAGATCTCAGAGTAAGAACAA		
Db	437 Asp Ile Arg Gln Ser Gly Ser Gly Ser Gly Asp Ser Asn Lys		
Qy	64 TATGTGAACTTGATTTCATGGAAACCTCGTCATCCCTCTGATG		
Db	457 Lys Ser Lys Ser Arg Ser Lys Ser Gly Ser Lys Ser Ser L		
Qy	124 GCTTCGTATAATTGCAACACAGGCTGAGGTCTGGGG	-	-
Db	477 His Asn Arg Asn -	-	-
Qy	184 AGCAGTGCGAGCACTCTGACCTCTGAGCTGAGTGAAGT		
Db	487 Ser Arg Ser Lys Glu Ile Arg Asp His Glu Asn Val Lys Glu Lys SG		
Qy	244 AGGGAGCAACCAACAAAAAAGCAGACTCCCCCAGGCCCTCAG		
Db	507 Lys Glu Lys Asp PGLnGlu Arg Ser Arg Ser Lys Glu Lys Ser L		
Qy	304 TCCAACTCCGATTCAAGATGAAACTGGAAATGAAATTTTTGG		
Db	525 Ser Lys Ser Arg His Glu Ile Ser Lys Ser Lys Glu Lys A		
Qy	364 ATAAGCAAAACAAAGCAATGCTGCCAAACTCATGTCATGAT		
Db	543 ----Gln Ser Arg Ser Arg Glu Cys Asp Ile Thr Ile Thr Gly His AA		
Qy	424 TCGTTCCGTTGGAAAAGCATCCCCCTCCAGGCTTCGACTCACAA		
Db	561 Arg Thr Arg Glu Arg -----Ser Arg Ser Arg Asp Arg S		
Qy	484 CGTAGATTCCGGGTTGGCTTCGCTTCAGGCTCAGG-----		
Db	578 Arg Thr His Asp Arg Asp Arg Ser Arg Ser Lys Glu Tyr His AA		
Qy	523 CGGAGAGCTGTCCTACAGGTCAAGGTCCGGATCCTCG		
Db	598 Tyra Garg Arg Gyl Arg Ser Arg Ser Arg Glu Arg -----		
Qy	583 CCCATGGRGICAGCCGGTITKGARQRTMWMGTAATGTTGGTGA		
Db	612 Pro Pro Gly Arg Ser Arg Ser Lys Asp -----A		
Qy	643 GATGGTACATGAGAATGAGATTAACGCCAGTGGAGAAATTACAGAGGCC		
Db	627 Asp Ser Arg Ser Ser Gly Ser Gly Ser Gly Ser Arg Asn L		
Qy	703 CTTCGGCATATAATTGCGCCAGTGGAGAAATTACAGAGGCC		
Db	644 -----Tyra Garg Asp Lys Ser Ser His AA		
Qy	763 AGCAATTCTCGAGGAGAGATATAACCGTTCATGGG-----T		
Db	658 Ser Glu Ser Gly Ser Arg Met - Tyr Ser Lys Ser Arg Asp His		
Qy	820 CGTCAAGAGACTATGAT		
Db	678 Arg Glu Lys SAla sp Arg Asp Gln Ser Pro Phe Ser Lys I		
Qy	862 GACTGCTGGGGTTTCAGGGCAATTGTCAGCCCTGCGCTTC		
Db	698 Asp -----Asp Glu Leu Lys Ser Ser Met Leu I		
Qy	922 GAGGTCAAGGATGTCGTCGCTGGATCCGAAC 951		
Db	713 Lys Ile Arg Ser Ser Gly Ser Gly Ser Gly Ser Gly 722		

QY 550 AGGTCCGGATCCTGGTCCCTGACGCTCTACCCATGGAGGCCAGTTKGARKMT 609
 Db 303 ArgSerArg-----SerArgSerTyrSerProArgArgProSerProArgArg 319
 QY 610 MWGTACATGTTGTTGAGAAGAGGAGAGGGATGGATGGCATAGATGAAGATSGACCTG 669
 Db 320 ArgProSer-----ProArgArgGlyProArgMetProProPro ----- 335
 QY 670 CCCAGAGCGCTCGTCAGATCATCGTG 699
 Db 336 ProArgHisArgArgSerArgSerProVal 345

RESULT 6
 US-09-188-930-185
 ; Sequence 185, Application US/09188930A
 ; Patent No. 6105052
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James Greg
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 ; TITLE OF INVENTION: and Methods For Their Use
 ; FILE REFERENCE: 11000-1011C1
 ; CURRENT APPLICATION NUMBER: US/09/188,930A
 ; CURRENT FILING DATE: 1998-11-19
 ; NUMBER OF SEQ ID NO: 348
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO: 185
 ; LENGTH: 536
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-188-930-185

Alignment Scores:
 Pred. No.: 0.00472
 Score: 110.00
 Percent Similarity: 37.88%
 Best Local Similarity: 21.86%
 Query Match: 5.61%
 DB: 3

US-10-046-935-2234 (1-1116) x US-09-188-930-185 (1-536)

QY 172 TGTAGGACCGC-----AGCAGTCAGGCC 198
 Db 250 CysArgProArgProArgAlaCysAlaSerLeuLeuGlyLeuNetGlnArgcystRphis 269

QY 199 TCTGACCT---CTCAGGGGGATGAAGTTCCAGGGGGATACCAGGGAGCAAC 255
 Db 270 AlaAspPTGlnAlaArgProThrPheGlnGluLeuSerGluLeuAspLeuCys 289

QY 256 AACAAAAGCAGG-----TCCGGCCAGCCTCAGAAATTCTGTGACT 300
 Db 290 GluLysProAspGluValuLysAspLeuAlaHisGluProGlyGluLysSerLeu 309

QY 301 GATCCCAACTCCGATTCAAGATGAAGTGGATGAATTTCGGAAAGGGCTTA 360
 Db 310 GluSerLysSerGluAlaArgProGluSerSerArg-----LeuLysBargAlaSerAla 327

QY 361 AATATAAAGCAAACAAAGCAATGCTTGCACAACTCATGTCGAATTAGAACG-----414
 Db 328 ProProPheAspAsnAspSerSerLeuSerGluLeuSerGlnLeuAspSerGlyIle 347

QY 415 TTCCCTGGCTCGTCGCGAGAACATCCCTCCAGGCTCCACTCACATAAGAGA 474
 Db 348 ProProArgLeuLeuLeuSerGlyProGluGluUserArgSerSerSerGluCysLysLeu 367

QY 475 CGGGAAAG-----CGTACATTCGGGRTGTTCCAGGAGAACCTGTGACGG 525
 Db 368 ProSerSerSerGlyLysArgLeuSerGlyValSerSerAlaPheSer 387

Qy 526 AGAGCTCGTCTCTTACCGGTCAGGCCCCGATCCTCGGCCCCCTGACGCTCTACCC 585
 Db 388 SerArgGlySerLeuSerGluAlaSerGlyAspLeuGlyPro 407
 Qy 586 ATGGRGAGGCCAGTTKGARKMTMWGTACATGTTGTCGAGAANGAGGAGACCGTGGAT 645
 Db 408 ThrAsp-----IleGlnLysLysLysLeuValAsp 417

Qy 646 GGCTACATGATGAGATGACCTGCCTGCCAGAGGCCCTCGTCAGA-----690
 Db 418 AlanLeuSerGlyAsp-----ThrSerArgLeuMetLysLeuGlnProGln 434

Qy 691 -----TCATCGTGACCCCTCCGGCATATAATTGCCCACTGGAA 729
 Db 435 AspValAspLeuValLeuAspSerSerAlaSerLeuLeuIleLeu-----AlaVal 451

Qy 730 GAAATTACAGGAGGAGTGGAGAAC-----CTCTGCAGCAATTCTCGAGAGAAAGATA 783
 Db 452 GluAlaGlyGinGluLysValLysTrpLeuLeuLeuAsnAlaAsnProAsnLeu 471

Qy 784 TATACACGTCACGGGCTACTCTGTCATCAANCGCTGAGA-----828
 Db 472 ThrAsnArgLysGlySerThrProLeuLysMetAlaValGluArgLysGlyArgGlyIle 491

Qy 829 -----ACTATTGATAACAAAAAACACTGAGAACCCAGACTGTG 870
 Db 492 ValGluLeuLeuAlaLysLysSerValAsnAlaLysAspGluAspGlnTrp 510

RESULT 7
 US-09-312-2B3C-185
 ; Sequence 185, Application US/0912283C
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James G.
 ; TITLE OF INVENTION: Compositions Isolated from Skin Cells
 ; TITLE OF INVENTION: and Methods For Their Use
 ; FILE REFERENCE: 11000-1011C2
 ; CURRENT APPLICATION NUMBER: US/09/312,283C
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NO: 425
 ; SOFTWARE: FastSBQ for Windows Version 4.0
 ; SEQ ID NO: 185
 ; LENGTH: 536
 ; Matches: 61
 ; Conservative: 43
 ; Mismatches: 111
 ; Indels: 64
 ; Gaps: 12

Alignment Scores:
 Pred. No.: 0.00472
 Score: 110.00
 Percent Similarity: 21.86%
 Best Local Similarity: 21.86%
 Query Match: 5.61%
 DB: 4
 US-09-312-2B3C-185

QY 172 TGTAGGACCGC-----AGCAGTCAGGCC 198
 Db 250 CysArgProArgProArgAlaCysAlaSerLeuLeuGlyLeuNetGlnArgcystRphis 269

QY 199 TCTGACCT---CTCAGGGGGATGAAGTTCCAGGGGGATACCAGGGAGCAAC 255
 Db 270 AlaAspProGlnAlaArgProThrPheGlnGluLeuSerGluLeuAspLeuCys 289

QY 256 AACAAAAGCAGG-----TCCGGCCAGCCTCAGAAATTCTGTGACT 300
 Db 290 GluLysProAspGluValuLysAspLeuAlaHisGluProGlyGluLysSerLeu 309

QY 301 GATCCCAACTCCGATTCAAGATGAAGTGGATGAATTTCGGAAAGGGCTTA 360
 Db 310 GluSerLysSerGluAlaArgProGluSerSerArg-----LeuLysBargAlaSerAla 327

QY 361 AATATAAAGCAAACAAAGCAATGCTTGCACAACTCATGTCGAATTAGAACG-----414
 Db 328 ProProPheAspAsnAspSerSerLeuSerGluLeuSerGlnLeuAspSerGlyIle 347

QY 415 TTCCCTGGCTCGTCGCGAGAACATCCCTCCAGGCTCCACTCACATAAGAGA 474
 Db 348 ProProArgLeuLeuLeuSerGlyProGluGluUserArgSerSerSerGluCysLysLeu 367

QY 475 CGGGAAAG-----CGTACATTCGGGRTGTTCCAGGAGAACCTGTGACGG 525
 Db 368 ProSerSerSerGlyLysArgLeuSerGlyValSerSerAlaPheSer 387

Qy 526 AACAAAAGCAGG-----CGTACATTCGGCCTCAGGAGAACCTGTGACT 300
 Db 290 GluLysProAspGluGluValuLysAspLeuAlaHisGluProGlyGluLysSerLeu 309

Qy 301 GATCCCACTCCGATTCAAGATGAAACTGGATTTGGAAAGGGCTTA 360
 Db 310 GluSerIleSerGluAlaLargProGlutserSerArg-----LeuIleArgAlaSerAla 327
 Qy 361 AATAAAGCAAACAGCAATGCTTCGAAACTTGTCAATTAGAACG---- 414
 Db 328 ProProheAspAlaAspCysSerLeuSerGluLeuAspSerGlyIle 347
 Qy 415 TTCCCTGGCTCGTTCGTTGAAAGCATCCCTCCAGCTCCACTCAATAAGGAGA 474
 Db 348 PheProArgLeuLeuLysProGluGluLeuSerArgSerSerGluCysLysIeu 367
 Qy 475 CGCGGAAGG-----CGTACATTCCGGGTTGCTCCAGGAAACCTGAAACGG 525
 Db 368 ProSerSerSerGlyIleArgLeuSerGlyValserSerAlaPheSer 387
 Qy 526 AGAGCTCGGCCCTTACAGGTCAAGGRCGGATCCTGGGTCCTTGACGCTCTAACCC 585
 Db 388 SerArgGlySerLeuSerLeuSerPheGluArgGluAlaSerThrGlyAspLeuGlyPro 407
 Qy 586 ATGGRGAGGCGCAGTTGKARYTMWGGTACATGTTGGCTGAGAAAGGAGAACGGTGGAT 645
 Db 408 ThrAsp-----IleGlnGlyIleSerLeuValAsp 417
 Qy 646 GGCTACATGAATGAGAGAACCTGCCAGAAGCCGTCGCTCCAGA----- 690
 Db 418 AlaIleIleSerGlyAsp-----ThrSerArgLeuMetIleLeuGlnProGln 434
 Qy 691 -----TCATCCGPGACCCCTTCGCGATAATTCGCCAGTGAA 729
 Db 435 AspValAspIleValLeuAspSerAlaSerLeuLeuHisLeu-----AlaVal 451
 Qy 730 GAAATTACAGAGGGAGGAACTCTGAGAGAAAGATA 783
 Db 452 GluAlaGlyIleInGluGlyValIleSerLeuAsnAlaAsnProAsnLeu 471
 Qy 784 TATAACCGTTCACGGCTCTACTGGCTCTACTGTCATCAATGCCGTCAGAAG----- 828
 Db 472 ThrAsnArgIleGlySerThrProLeuHisMetAlaValGluArgGlyIle 491
 Qy 829 -----ACTATTGATAACCAAAACAACTGAGAAACCCAGACTGTGTTG 870
 Db 492 ValGluLeuLeuAlaArgLysThrSerValAsnAlaLysAspGluAspGlnTrp 510
 RESULT 8
 US-08-791-115B-5
 Sequence 5, Application US/08791115B
 i GENERAL INFORMATION:
 i APPLICANT: Steck, Peter
 i APPLICANT: Pershouse, Mark A.
 i APPLICANT: Jaser, Samar
 i APPLICANT: Yung, W.K. Alfred
 i APPLICANT: Tavtigian, Sean V.
 i TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
 i NUMBER OF SEQUENCES: 27
 i CORRESPONDENCE ADDRESS:
 i ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
 i STREET: 555 Thirteenth Street, N.W., Suite 701-E
 i CITY: Washington
 i STATE: DC
 i COUNTRY: USA
 i ZIP: 22204
 i COMPUTER READABLE FORM:
 i MEDIUM TYPE: Floppy disk
 i COMPUTER: IBM PC compatible
 i OPERATING SYSTEM: PC-DOS/MS-DOS
 i SOFTWARE: Patent In Release #1.0,
 i CURRENT APPLICATION DATA:
 i APPLICATION NUMBER: US/08/791,115B
 i FILING DATE: 30-JAN-1997
 i CLASSIFICATION:


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; SEQ ID NO 31991_
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-2522-991A-31991

Alignment Scores:
Pred. No.: 0.0122
Score: 105.00
Percent Similarity: 36.36%
Best Local Similarity: 24.13%
Query Match: 5.35%
DB: 4

US-10-046-935-2234 (1-1116) x US-09-2
Qy 13 CGCGTGCAGCAGAAAGATCTCTG
Db 62 ArgValProProSerAlaAsp
Qy 73 TTGATTCCATGGAAACCTCTGTC
Db 82 AlaProPheSerItpProAsnSe
Qy 133 ATTTCATCAAACAGGAGGTCTGCA
Db 102 LeuIleLeuIleAsnGlyLeu--
Qy 193 AGCACTCTGACACTCTCGAGGT
Db 121 ThrSerSerLeuProValProLeu
Qy 253 ACCAACAAAAAGCAAGTCCCCG
Db 141 Ser----pheAlaserSerArg
Qy 304 TCCAACCTCCGATTCAAGAGATGA
Db 159 SerCysSerProSerAlaSerPro
Qy 361 ----
Db 179 LysAlaArgProArgValThrCys
Qy 391 AAACCTATGTTCTGAATTAGAAAGG
Db 199 LysAsnHisSerGlnThrLysSer
Qy 439 ---CATCCCCCTCCCC
Db 218 SerThrAlaLeuHisSerValPro
Qy 487 ACATTCGCCGGTGCTGCCGTCAG
Db 233 ThrValSerGly--ArgSerArg
Qy 547 TCAAGTCCCGATTCCTCGGTCC
Db 252 AlaArgSerArgAlaValSerSe
Qy 598 ATGTTKGARKMTMMNGTACATGTT
Db 272 ProGlyAsn----
Qy 658 GAAGATGACCTGCCAGAAACCGT
Db 286 ---SerArg
Qy 718 CGCCCAAGTGGAGAAATTACAGRA
Db 292 ----
Qy 778 AAGATATAAACCGTICA 795

```

RESULT 13

US -09-252-991A-27111 Application US/09252991A

Sequence 27111, Application US/09252991A

PATENT NO. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenstein et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107198-136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27111

LENGTH: 679

TYPE: PRT

ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-27111

Alignment Scores:			
Pred. No.:	Score:	Length:	Matches:
	0.0199	679	679
	105.00	70	70
	Percent Similarity: 40.43%	Conservative: 25	
	Best Local Similarity: 29.79%	Mismatches: 80	
	Query Match: 5.35%	Indels: 60	
DB:	4	Gaps: 13	

US-10-046-935-2234 (1-1116) x US-09-252-991A-27111 (1-679)

QY	415	TTCCCTGCTGGTCCGTGGAGACATCCCTCCAGCTCCACTACAATCAAGGAGA	474
Db	323	PheProAlaSerSerArgThrArgHisSerAlaProProArgArgProGlyAlaArgArg	342
QY	475	-----CCGCGAAAGGGT-----ACATTCGCCGGTGCTTCAGGAGA	513
Db	343	AlaArgProSerProLysGlyArgGlyAspTPAlaGlyProGlyAlaProAlaArgArg	362
QY	514	AACCTGAAAGGAGACTCGT-----CCTCTTACAGCTCAAGT-----	553
Db	363	GlyArgGluGlyArgAlaArgAlaGlyLeuProAlaLysGlyAlaGlySerPro	382
QY	554	-CCCGGATCTCCGGTCCCTGACGCTTACCCATGGRGAGCCAGTTKGARKMWNWG	612
Db	382	ralAlysSerProGlyPro-----	388
QY	613	TACATGTTGGTGGAGAAAGGAGACGTGATGGCTACATGAATGGAGATGACCT-----	669
Db	389	-----AlaArgGly-SerArgGlyTrpProGlyValArgTrpProAlaIle	404
QY	670	CCCGAAGGCGCTGCTCAGATCATCGTGCACCCCTCGCATATAATTGCCCAAGTGCGAA	729
Db	404	rgArgGlyProSerArgGlySerAlaArgArgAlaArgAlaArgProAlaAlaAlaPro	424
QY	730	GAAATTACAGGGAGGTT-----GGAACCGTGTGCGACANTTCGAGAGAAATA	783
Db	424	rgArgAlaProSerHisCysArgGlyProProGlyProGlyArgSerAlaArgSerArg-----	442
QY	784	TATACCGTGTACTGGCTTACATGCTGCTTACATGCTGCTGCGAAACCCAGACTGCTGGCGCTGCGA	879
Db	443	-IleArgArg-----SerAlaIleSerTrpProGlyAlaGlyAlaIleAlaProAlaIle	476
QY	880	GGCCAGTGTGCCCCCTGCGCTTGGAGAGAGCTATGCTGAGAGCTGCGATCTGCTG	939

Db 476 GCYBCysSerProAlaHisAla--GluLeuValGlnAlaArgArg-----ValVa 492
 Qy 940 CTGGATCCGAACtGCATGCCCGCTTGTGAGGAATCTGCA-----ACTGGAGTTTC 993
 Db 492 lGluLeuArgLametValArgValAlaSerAlaValGlyThrValLeuIar 512
 Qy 994 TGCAGGAGCCGAGATGGACGGTGTGCACTGGGTCC 1030
 Db 512 GluGluLysArgLysLeuAspGlyLeuHisArgGlyAla 524

RESULT 14
 US-09-418-780A-1
 ; Sequence 1, Application US/09418780A
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Michael H.
 ; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
 ; FILE REFERENCE: 06501-043001
 ; CURRENT APPLICATION NUMBER: US/09/418, 780A
 ; CURRENT FILING DATE: 1999-10-15
 ; PRIOR APPLICATION NUMBER: PCT/JP98/01782
 ; PRIOR FILING DATE: 1998-04-17
 ; PRIOR APPLICATION NUMBER: JAPAN 9/116402
 ; PRIOR FILING DATE: 1997-04-18
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 947
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-418-780A-1

Alignment Scores:
 Pred. No.: 0.0359 Length: 947
 Score: 103.50 Matches: 71
 Percent Similarity: 33.44% Conservative: 37
 Best Local Similarity: 21.98% Mismatches: 90
 Query Match: 5.28% Indels: 125
 DB: 4 Gaps: 16

US-10-046-935-2234 (1-1116) × US-09-418-780A-1 (1-947) 93

Qy 64 TATGTGAAGTGATTTCATGGAAACTCG-----
 Db 388 TyrIleGlyThrAspIleIleGlyLysGluAsnThrAsnGluAlaSerSer 407
 Qy 94 -----TCATCCTCTATGAGAGTTGACAGCTTGTCTGATAATTGCAAACACG 147
 Db 408 GluGlyAsnSerSerAspSerGluAspGluAspGlyValLys----- 421
 Qy 148 AGGCTGAGTCAGTCAGTCGGAAAGCTGTAGGACCCGAGCTGCAACTCTGACCT 207
 Db 422 ArgLeuAlaLysLeuGlnGlnLeuLysAlaValAlaHisGln-----Gln 436
 Qy 208 CTCAGGCTGGCCATGAAAGTTCAGCCGGACTACCGGGAGCAACCAAAAGCA 267
 Db 437 LeuGlnValLeuSerGlnValProPheArgLys-----LeuAspLysLys 452
 Qy 268 GAG-----TCCCGCCGCCCCCTAGAGAAATTCTGTGACTGATTCCAACCTCGAT-----315
 Db 453 GluLysSerLysLysGluLysLeuLysSerGluLysValAsnAsnSerGluAsnProArg 472
 Qy 315 ----- 315

Qy 403 GAATTAGAAAGCTCCCTGGCTGGAGA-----CATCCCCCTCCGGCTCC 456
 Db 525 -----LeuProDlyAspLysLeuGlyArgValValHisIleIle----- 537
 Qy 457 GACTCACAACTAACAGAGACCGGAAGGGTACATTCGGGGTGTGCTCCAGGAGAAC 516
 Db 538 -----GlnSerArgGluProSer-----LeuSerAsnSerAsn 548
 Db 517 CCTGAAACGG-----
 Qy 549 ProAspGluIleGlyIleAspPhyGluThrLeuArgGluLeuGlu 568
 Db 526 -----AGGCTCGTCCTCTACAGGCTAACGTCAGGATCCGATCCTC 564
 Qy 569 LysTrpValSerAlaCysLeuArgLysArgProLeuLysProProAlaLysLysIleMet 588
 Db 565 GGTRCCCTTGACGCTCTACCCATGRRGAGAGCCAGTTTGKARQNTMWWGTPACATGTTGTRG 624
 Qy 589 MetSerLysGlnGluLeu-----HisSerGlnLysLysGlnGluLeu 603
 Db 625 AGAAAGAGGAGAACGACATGAGATGACCTCCGGCAAGGGTGC 684
 Qy 604 LysArgLeuAspValAsnAspGlnLeuAsnSer-----ArgLysArgGln 619
 Db 685 TCCAGATCATCCGTAATGACATTAATTGCCCACTGGAAATTACA-----738
 Qy 620 ThryLysSerAspLysProValAsnAspGlnLeuAsnSer-----LysAlaValGluAsnValSerArgLeu 637
 Db 739 GAGGAGGAGTTGGAGAACGCTGCGCAATTCTCGAGAGATATAACCGTICACTG 798
 Qy 638 SergiuUserSerSerSerSerSerSerSerSerSerSerSerAspLeu 657

Qy 799 GGCTCTACT 807
 Db 658 SerSerSer 660

RESULT 15
 US-09-392-714-23
 ; Sequence 23, Application US/09392714A
 ; Patent No. 6686147
 ; GENERAL INFORMATION:
 ; APPLICANT: Scanlan, Matthew J.
 ; APPLICANT: Gure, Ali O.
 ; APPLICANT: Williamson, Barbara
 ; APPLICANT: Chen, Yao-Tseng
 ; APPLICANT: Old, Lloyd J.
 ; TITLE OF INVENTION: Cancer Associated Antigens and Uses
 ; TITLE OF INVENTION: Therefore
 ; FILE REFERENCE: L0461/7062
 ; CURRENT APPLICATION NUMBER: US/09/392,714A
 ; CURRENT FILING DATE: 1999-09-09
 ; EARLIER APPLICATION NUMBER: PCT/US98/14679
 ; EARLIER FILING DATE: 1998-07-15
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 23
 ; LENGTH: 947
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-392-714-23

Alignment Scores:
 Pred. No.: 0.0359 Length: 947
 Score: 103.50 Matches: 71
 Percent Similarity: 33.44% Conservative: 37
 Best Local Similarity: 21.98% Mismatches: 90
 Query Match: 5.28% Indels: 125
 DB: 4 Gaps: 4
 Alignment Scores:
 Pred. No.: 0.0359 Length: 947
 Score: 103.50 Matches: 71
 Percent Similarity: 33.44% Conservative: 37
 Best Local Similarity: 21.98% Mismatches: 90
 Query Match: 5.28% Indels: 125
 DB: 4 Gaps: 16

US-10-046-935-2234 (1-1116) × US-09-392-714-23 (1-947)
 Qy 64 TATGTGAAGTGATTTCATGGAAACTCG-----
 Db 473 LysMetCysGluGlnMetArgLeuLysGluLysSerLysArgAsnGlnProLysArg 492
 Qy 316 -----TCAGAAGATGAAAGTGTGAA-----ATGAAATTTC 342
 Db 493 LysGlnGlnPheIleGlyLeuLysSerGluLysSerGluAspAsnAlaLysProMetAlaTy 512
 Qy 343 TCGGAGAAAAGGCTTAAATAAAGGAAAAAACAAAGCAATGTTGGAAAATCTCATGCT 402
 Db 513 AspDluLysArgLysArgLysLeuSerLysLeuSerLysLeuAsnLys----- 524

Db 388 TyrIleSerThrAspIleThrGluThrThrGlyArgGluAsnThrAsnGluAlaSerSer 407
 Qy 94 -----TCATCCTCTATGACAGTGTGGTGTGACAGCTTGTCTGCTATAATTGCAAAACAG 147
 Db 408 GluGlyAsnSerSerAspSerGluAspGluArgVallys----- 421
 Qy 148 AGGCTGCACTGAGTCACTGGAGGTGTAGGACCCGAGCCAGCAGCTGAGGACTCTGACCT 207
 Db 422 ArgLeuAlaLysLeuGluGlnLeuLysAlaValIleGln-----Gln 436
 Qy 208 CTCAGGTGGCGATGAGTTCAGGTTGAGCTTGAGGAGTACAGGGAGCAACCAAACAGCA 267
 Db 437 LeuGlnValLeuSerGlnValProPheArgLys-----LeuAsnLysLysLys 452
 Qy 268 GAG-----TCCCAGCTAGAGAACTCTGAGACTATTCCAACACTCGAT----- 315
 Db 453 GluLysSerLysLysGluLysGluLysValAsnSerAsnGluAsnProArg 472
 Qy 315 ----- 315
 Db 473 LysMetCysGluGlnMetArgLeuIleGluIleSerLysArgAsnGlnProLysArg 492
 Qy 316 -----TCAGAGATGAAGTGC-----ATGATTTC 342
 Db 493 LysGlnGlnPhenylGlyLeuLeuSerGluAspGluAspAsnAlaLysProMetAsnTyR 512
 Qy 343 TTGGGAAAGGGCTTAATTAAGAACAAAAGCATGCTGCAAAACTCATGCTT 402
 Db 513 AspGluIleSerGlnLeuAsnIleAsnLys----- 524
 Qy 403 GAATTAGAAAGCTTCCCTGCCTCGCTCCGGAGA-----CATCCCCCTCCAGGCTCC 456
 Db 525 -----LeuProGlyAspLysLeuGlyArgValValHisIleIle----- 537
 Qy 457 GACTCACAACTCAAGGAGACGCCAGGGCTACATTCGGGTGTTGCTCAGGAGAAC 516
 Db 538 -----GlnSerArgGluProSer-----LeuSerAsnSerAsn 548
 Qy 517 CCTGAAACGG----- 525
 Db 549 ProAspGluIleGluIleAspPheGluThrLeuIleArgGluLeuGlu 568
 Qy 526 -----AGAGCTCTCTCTCTTACAGGTCAAGGTCAGGTCGGATCTC 564
 Db 569 LysTyrValSerAlaCysLeuWgIlysArgProLeuIleSerProAlaLysIleMet 588
 Qy 565 GGTCCTCTGACGCTTACCATGGRGAGCCAGTTKGARKMTMTCATGTTGTTG 624
 Db 589 MetSerLysGluGluLeu-----HisSerGlnLysGlnGluLeuGlu 603
 Qy 625 AGAAAGAGAACCCGTTGACCTGCTACATGAAAGATGACCTGCCAGTGGAAATATACA 684
 Db 604 LysArgLeuLeuAspValAsnAsnGlnIleAsnSer-----ArgLysArgGln 619
 Qy 685 TCGAGATCATCGTGCACCTTCGGCATATAATTGCCAGTGGAAATATACA 738
 Db 620 ThrLysSerAspIleThrGlnProSer-----LysAlaValGluAsnValSerArgLeu 637
 Qy 739 GAGGAGGAGTGGAGAACGTCAGCAATTCTCGAGAGAAAGATATAACGTTCACTG 798
 Db 638 SerGluUserSerSerSerSerSerSerSerSerSerSerSerSerAspLeu 657
 Qy 799 GGTCTACT 807
 Db 658 SerSerSer 660

BLANK